

QY 806 AYKGLLVGVYMAWETRRHVKIPALNDSOYIGVSVVITSAlVVVLANLISERVTLAF 865
Db |||||::|::|||::| |||||::|||::|||::| |::|::|::|
661 aykglmlfgyflawetrvnsipalndskyigmvnyvgimciigaavsfldrqpnhvf 720
QY 866 ITITALILTSTTATLCLFIPKLDIWARNDIIDPVIHSMGLKMECNTRRFVVDDBRELQ 925
Db : : : : |||::||| : : : : | : : : : |
721 civalvliifcstltclvfpkl-----itltnpdaatqnrffq 760
QY 926 YRVEVONRVYKKEIQALDAEIRKLERLLESGLTSTTT--SSSTSLLTG-----GGHLKP 979
Db : : : : ||| : : : : | : : : : | : : : : |
761 f---tqng--kk-----edsktstsvtsvngqastsrleglqsenhrlrm 799
QY 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011
Db : : : : ||| : : : : | : : : : | : : : : |
800 kitelkdleevlmqldtpekttyikqnhyqelndillsignfstdgkailknhl-- 857
QY 1012 VLPPVIPRASWPSAE 1026
Db : : : : | : : : : |
858 ---dqpqlqwtte 869

Search completed: April 30, 2002, 10:00:46
Job time: 589 sec

Db 661 aykglmlfclawetnrvipalndskylgmsvnygmciigaavsfldrqpqvaf 720
QY 866 ITIVALTSTATLCLLFIKPLHDIWANDIIDPVIHSMGLKMECNTRFRVVDRELEQ 925
Db 721 civalvifefstltclvfpkl-----itlrtpdaatqnrfrq 760
QY 926 YRVEQNRVYKKEIQALDAERIKLERLLESGLTTSTTT--SSSTSLLTG-----GGHLKP 979
Db 761 f---tgnq--kk-----edsktstsvtsvngdastsrleglqsenhrirm 799
QY 980 ELT-----VTSGISOTPAASK-----NRTPSISG---ILPNLLLS 1011
Db 800 kiteldkdvtnqigdtpekttyikqnhqyelndilslngftestdggkailknhl-- 857
QY 1012 VLPPVPIPRASWPSAE 1026
Db 858 ---dqpqlqwnite 869
RESULT 15
AA770327
ID AAY70327 standard; Protein; 940 AA.
XX
AC AAY70327;
XX
DT 21-JUN-2000 (first entry)
XX
DE Rat gamma amino butyric acid receptor, GABA-B-R2 protein.
XX
KW Gamma amino butyric acid; GABA-B-R2; rat; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antiasthmatic; antiaddictive;
KW uropathic; analgesic; antitussive; agonist; neuroprotective; nociceptive;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX
OS Rattus sp.
XX
FH Key
FT Peptide
FT 1..40 Location/Qualifiers
FT /label= Signal_peptide
FT Protein
FT 41..940 /label= Mature_rat_GABA-B-R2_receptor_protein
FT Domain
FT 480..503 /label= Transmembrane_domain-I
FT Domain
FT 517..544 /label= Transmembrane_domain-II
FT Domain
FT 555..577 /label= Transmembrane_domain-III
FT Domain
FT 596..618 /label= Transmembrane_domain-IV
FT Domain
FT 654..676 /label= Transmembrane_domain-V
FT Domain
FT 690..711 /label= Transmembrane_domain-VI
FT Domain
FT 719..743 /label= Transmembrane_domain-VII
XX
XX WO200012692-A1.
XX
XX 09-MAR-2000.
XX
XX 27-AUG-1999; 99WO-US19651.
XX
XX 27-AUG-1998; 98US-0141760.
XX 16-OCT-1998; 98WO-US22033.
XX 04-NOV-1998; 98US-0186664.
XX 15-DEC-1998; 98US-0211755.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
XX Jones KA, Laz TM, Borowsky B;
XX

DR WPI: 2000-246751/21.
XX N-PSDB; AAZ51400.
PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
PT detecting receptor agonists useful for treating e.g. asthma,
PT incontinence, and Alzheimer's disease -
XX Claim 12; Fig 4; 260pp; English.
PS
XX The present amino acid sequence is the rat GABA (gamma amino butyric
CC acid)-B-R2 receptor protein, isolated from rat hypothalamic cDNA library.
CC This sequence is used to construct the plasmid BO-55 (ATCC.No. 209104).
CC GABA-B is a major inhibitory neurotransmitter, the receptors of which are
CC widely distributed throughout the central nervous system. GABA-B-R2
CC receptor has anticonvulsant, antiasthmatic, uropathic, analgesic,
CC antitussive, antiaddictive, nociceptive and neuroprotective activity.
CC GABA-B-R2 receptor agonists may be used to treat spasticity, asthma,
CC incontinence, drug addiction, Alzheimer's disease, decrease nociception
CC and as an antitussive agent. Transgenic animals with altered GABA-B-R2
CC levels may be used to determine the physiological effects of varying
CC levels of GABA-B-R2 receptor activity.
XX Sequence 940 AA;
SQ
Query Match 15.9%; Score 1065.5; DB 21; Length 940;
Best Local Similarity 29.5%; Pred. No. 1.6e-85;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;
QY 155 LGLFELSTGRPRPDGLSELGAATMAVEHNRKRLPGYTELVNTDQDGPVGVDVF 214
Db 57 imglmpitkeavagsigrvlpavelaiegirneslirpyfidrlrlydtecdnkykaf 116
QY 215 FHAIYQPSRMVWLGLSACSEVTESLAKVVPYVNIQVSPGSTSPALSDREERPFYRT 274
Db 117 ydaikygn--hlmvfggvcpvtsiaeslqgnvlqslfaatlvpdadkkyppfirt 174
QY 275 VAPDSSHNPARIAFIRKFGWGTVTFSQNEVHSLAVNNLVLEAANISCAAITFA-- 332
Db 175 vpsdnavnpaillklkhfrwrvgtltqdvqrfsevrndltgvygediesdesfnd 234
QY 333 -ATDFEQLLLRRTDTRIIGSFQELAPQILCEAVRLRMFGADYAWILHESGAPWMP 391
Db 235 pctsvek--lkgndvriilgfdqmaakvfccateesmfqkyqwigvypawwe 290
QY 392 D-----QRTACSNHELQAVENLIVVTHNSIVGNVNNYSGLNNHMFNSQLRKSAQPHG 446
Db 291 qvhveansrcrlrrsllaamegyi-----gvdfeplsskqiktisgktpqgyer 339
QY 447 Q-DGFGSGYGPRIISAATQSDSRRRRRRGVVGTSGGHLFPPEAISQYAPQTYDAVMAIALA 505
Db 340 eynsktrsgvp-----skfhgaydygiwviakt 367
QY 506 LRAAEHRRNEBOSKLDGFDYTRSDMAWEFLQOMGLHFLGVSGVPSFSGPDRVGTTF 565
Db 368 lgrametlhassrhriqgdnfnydhtlglkllnamnetnffvgvqvfrngermtlkf 427
QY 566 YQIORGLEPVALYYPATDALDFRCPRCPVKWHSQGVPIAKRVFKLRVATIAPIAFYTI 625
Db 428 tqfqsrevkvgeynavadtleiind---tlfqgseppkdktilleqlrkisiplyail 484
QY 626 ATLSVGIALAITFLAFNLHFKLKAIKLSPKLSNITAVGCIFFYATVILLGDHSLP 685
Db 485 saltilgiminasafflnknrdkllkmsppymnliilggmlsyasiffldgsfv- 543
QY 686 SAEDSFATVCTARVYLLSAGFSLAFSGMFAKTYRVHRIFRTGSGVDFKMLQIQLILLY 745
Db 544 -sektfetlctvrtwiltvgttafgamfaktwrvaifknv--kmkkkiikdkllviv 600
QY 746 GGLLLVALLVTLWVTDPMERHLNLTLEISATDSRVVYQPOVEKCSQHTQWLSVLY 805
Db 601 ggmlldilclicqavdprrrtverysmepdpagrdisrpllehcenhtwtlwgiv 660

Db 429 tqfadsrevkgeynavadtieind---tirqgseppkdktiileqlrkisplpyl 485

QY 626 ATLSVGIATLAFNLFKKAIAKLSPPKLSNITAVGCFYVAVVILLGLDHSFLP 685

Db 486 saltlginimasafllfnikrnqkllkmsspymlnlllgmlsyasiflfgldgsfv- 544

QY 686 SAEDSFATVCTARVYLLSAGFSLAFSGMFAKTYRVHRIFTRTGSVFKDKMLQDIQLILV 745

Db 545 -sektfelctvrtwiltvgvttafgamfaktwrhaifknv--kmkklkldqkllviv 601

QY 746 GGLLLVDALLVTLVWVTPDMEHRLNHLTLEISATDRSVVYQPOVEVCRSOHTOTWLSVLY 805

Db 602 ggmllidciliicqavdplrttrveksmepdpgardisirpllehcenhtmlwlgivy 561

QY 806 AYKGLLIVGVYMAWETHRVKIPALNDSQYIGSVSYVITSIAVVVLANLISERVTLAF 865

Db 662 aykglmlfclawetrvnsipalndskylgmsvnyngimciligaaavfltrdqpnvqf 721

QY 866 ITITALLTSTATLCLLFIPLKLDIWARNDIIDPVHSMGLKMECNRRFVVDRELO 925

Db 722 civalvlfestitclivfvpkl-----itlrnpdaatqnrrfq 761

QY 926 YRVEVQNRVYKKEIQALDAEIKRLERLLESLTSTTT--SSSTSLTG---GGHLP 979

Db 762 f---tqng--kk-----edsktscvtsvngqastsrleglgsenhrlrm 800

QY 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011

Db 801 kiteldkleevtmqldtpekttyikqnhygelndiinlgnftestdggkailknhl-- 858

QY 1012 VLPVPVPRASWPSAE 1026

Db 859 ---dqpqlgwntte 870

RESULT 13

AA228837

ID AAY28837 standard; protein; 943 AA.

XX AC AAY28837;

XX DT 17-JAN-2000 (first entry)

XX DE Human GABAB2 receptor protein.

XX KW Human GABAB2 receptor protein; human gamma-aminobutyric acid receptor;

KW metabotropic receptor; synaptic transmission; antibody; spasticity;

KW recombinant nucleic acid technique; motor control disorder;

KW therapeutic modulator; GABAB2 quantification; affinity purification.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Misc-difference 13 /note= "Corresponds to cng codon"

FT Misc-difference 942 /note= "No corresponding codon in seq ID no.1"

FT Misc-difference 943 /note= "No corresponding codon in seq ID no.1"

FT Domain 1..422 /label= Extracellular_domain

FT /note= "can be swapped with the portions of calcium

FT receptor for measurement of antagonist activity"

FT Domain 423..686 /label= Transmembrane_domain

FT /note= "can be swapped with the portions of calcium

FT receptor for measuring intracellular effects"

FT Domain 687..883 /label= Intracellular_domain

FT /note= "can be swapped with the portions of calcium

FT receptor for measuring intracellular effects"

XX PN W09951636-A2.

XX 14-OCT-1999.

PD

XX 02-APR-1999; 99NO-US07352.

XX 03-APR-1998; 98US-0080676.

PR (NPSF-) NPS PHARM INC.

PA Garrett JE, Simin RT, Busby JG, Stormann TM;

XX WPI; 1999-610994/52.

XX N-PSDB; AAX90919.

DR Novel nucleic acids, used to screen for specific modulators, e.g. for

DR treating spasticity or Alzheimer's disease

XX Claim 5; Fig 2A-2F; 78pp; English.

XX The present sequence is the human GABAB2 receptor protein. GABAB

CC receptors are metabotropic receptors that modulate synaptic transmission

CC in brain. GABAB2 is closely related to GABAB1a and GABAB1b. GABAB2

CC polypeptides are produced using recombinant nucleic acid techniques. They

CC are used to raise antibodies and to identify specific modulators of

CC GABAB2. These modulators are useful for treating spasticity, motor

CC control disorders etc. The antibodies are used as therapeutic modulators,

CC for GABAB2 quantification, affinity purification and to study synthesis,

CC structure and function of the receptor.

XX Sequence 943 AA;

XX Query Match 15.9%; Score 1066.5; DB 20; Length 943;

Best Local Similarity 29.5%; Pred. No. 1.3e-85;

Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;

QY 155 LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKLRLPGYTLVLTNDTQCDPGVGVDPR 214

Db 58 imglmpitkevakgsigrvlpavelaieqirneslirpyfldrllydtecdnaklkaf 117

QY 215 FHAIYTOPSTRVMVLGSGACSEVTESLAKVVPYVNIQVVSFGSTSPALSDRREPFYVRT 274

Db 118 ydaikypgn--himvfgvcpsvtsiaesiqgnvlqslfaattpvldakkkypffrt 175

QY 275 VAPDSSHNPARIAPIRKFGWGTVTTFQSONEEVHSLAVNNLVTELEAANISCAATITFA-- 332

Db 176 vpsdnavnpaillkllhyqwkrgvtltqdvgrfsevrndltgvlgyediesdtesfnd 235

QY 333 -ATDFEQLLLLTRETDFRIIGSFQSLAPQLICEAVRLRMFGADYAWILHESGAPWPP 391

Db 236 pctsavkk-----lkgndvriilgqfdqmaakvfccayeenmygskypwlpwypeswwe 291

QY 392 DQRT-----ACSNHELOLAVENLIVVSTHNSIVGNVNSYSGLNHMFNSQLRKQSAOPHG 446

Db 292 qvhteansrcrlrknllaamegyi-----gvdfepllskqiktisgktpqgyer 340

QY 447 Q-DGFGSGYGPRIISIAATQSDSRRRRRRVGVGTSGGHLFPEAISOYAPQTYDAYWAIALA 505

Db 341 eynnktrsgvp-----skfhgaydygiwviakt 368

QY 506 LRAAEHRRNEEQSKLDGFDYTRSDMAWEFLQMGKHLFLVGSGPVSFSGDPDRVGTAF 565

Db 369 lgrametlhassrhqrdqfnydhtlgrilnlnmetnffvgvqvvfrngermtklf 428

QY 566 YQIORGLLEPVALLYPATDALDFRCPRCPVKWHSQGVPIAKRVFKLRVATPIAPLAFYTI 625

Db 429 tqfadsrevkgeynavadtieind---tirqgseppkdktiileqlrkisplpyl 485

QY 626 ATLSVGIATLAFNLFKKAIAKLSPPKLSNITAVGCFYVAVVILLGLDHSFLP 685

Db 486 saltlginimasafllfnikrnqkllkmsspymlnlllgmlsyasiflfgldgsfv- 544

QY 686 SAEDSFATVCTARVYLLSAGFSLAFSGMFAKTYRVHRIFTRTGSVFKDKMLQDIQLILV 745

Db 545 -sektfelctvrtwiltvgvttafgamfaktwrhaifknv--kmkklkldqkllviv 601


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QY 155 LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKRLLPGYTLLELVNTDTCDDPGVGVDRF 214
Db 58 imglptkavaksgigrvlpavelaieqirnesllrpyfldrlrlydtecdnakglkaf 117
QY 215 FHAIYQTPSTRMVMMLGSGACSEYTESLAKVVPYWNIVQVSFGSTSPALSRRPEPFYVRT 274
Db 118 ydaikygnp--hlmgvggpcsvtsiaeslqgnwlvlsfaattpvladkkyppffrt 175
QY 275 VAPDSSHNPARIATIRKFGGTVTTTSQNEEVHSLAVNNLVTELEAANISCAATITFA-- 332
Db 176 vpsdnavnpaillkllkhygkwrgvtltdqgrfsevrnditgvlgyedleisdtessnd 235
QY 333 -ATDFKEQLLLRETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
Db 236 pctsavk----lkgndvriilqgfdqnaakvfccayeenmygskypwlpwyepswe 291
QY 392 DQRT-----ACSNHELQLAIVENLVVSTHNSIVGNVNSYGLNNHMFNSQLRKQSAQPHG 446
Db 292 qvhteanssrclrknlilaamegyi-----gvdfepilsskqiktsgktppqyer 340
QY 447 Q-DGFGSGYGPRIISAATQSDSRRRRRRGVCTSGHLFPPEAISQYAPQYDVAWAIALA 505
Db 341 eynnkrgvgp-----skfhgyaydgilwiakt 368
QY 506 LRAAEHWRNNEQSKLDGFDYTRSDMAWEFLQMGKHLHFLGVSGVPSFSGPDRVGTAF 565
Db 369 lgramethlhasrhqriqdfnydhtlgrilnamnetnfgvtgqvfvnrgermgtikf 428
QY 566 YQIQRGLEPVALYYPATDALDFRCPRCPVKWHSQVPTAKRVFKLURVATIAPLAFYTI 625
Db 429 tdfqdsrevkvgcyavadtieind---tirfgseppkdkliileqikslpysli 485
QY 626 ATLSSVGIATITFLAFNLFHFKLKAIKLSSPKLSNITAVGCCIFVYATVILGLDHDSTLP 685
Db 486 saltlglmmasafllfniknrnqklkmspynmnnliilgmslyasiflfigdgsfv- 544
QY 686 SAEDSFATVCTARVYLLSAGFSLAFGSMFAKTYRVHRIFTRTGSVFKDKMLQDILLY 745
Db 545 -sektfetictvrtwiltvgtytafgamtaktvrhvaifknv--kmkkkiikdqkllviv 601
QY 746 GGLLVADALLVTLVWVTDPMERHLNLTLEISATDRSVVYQPOVEVCRSOTOTWLSVLY 805
Db 602 gmlldilciliwqavdplrtvkeysnepdpagdisirpillehcenthmtiwigivy 661
QY 806 AYKGLLVGVYVMAWETRVHKVPALNDSQYIGVSVYSWVITSATVAVVLANLISERVTLAF 865
Db 662 aykglmlfgclawetrvnsipalndskygmsvynvgimciigaavsfldrqpvnqf 721
QY 866 ITITALILTSTATCLLPIPKLHDIAWRNDIIDPVIHSMGLKMECNTRFVVDDRELQ 925
Db 722 civalvifcstlclvfvpk1-----itlrtnpdaatqnrifg 761
QY 926 YRVEQNVYKKEIQALDAIEIRLERLLESGLTSTTT--SSSTSLTLC--GGHLKP 979
Db 762 f---tqnq--kk-----edsktcsvtsvnqastsrledlqsenhrlrm 800
QY 980 ELT-----VTSGISQTPAASK-----NRTPTSG---ILPNLLLS 1011
Db 801 kiteidkdelevmtmqldfpekttyikqnhqygelndilnlnfnftestdgkailknhl-- 858
QY 1012 VLPPIVPRASWPSAE 1026
Db 859 ---dgnpqlqwnnte 870
```

RESULT 12

AAB50088

ID AAB50088 standard; Protein; 941 AA.

XX AC AAB50088;

XX AC AAB50088;

DT 19-MAR-2001 (first entry)

XX

HG20 protein sequence.

Human; HG20; gamma-amino-butyric acid receptor; GABA-B.

Homo sapiens.

WO2000073788-A1.

07-DEC-2000.

30-MAY-2000; 2000WO-CA00638.

01-JUN-1999; 99US-0137025.

(MERI) MERCK FROSST CANADA & CO.

Ng G, O'Neil G;

WPI; 2001-049959/06.

N-PSDB; AAC91906.

Use of gabapentin, 1-(aminomethyl)cyclohexanecarboxylic acid, in assays for identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists

Claim 2; Fig 3; 85pp; English.

The present invention relates to a method for determining whether a substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a potential agonist or antagonist of the GABA-B receptor. The method comprises exposing cells to 1-(aminomethyl)cyclohexanecarboxylic acid (gabapentin) in the presence or absence of the substance under investigation. The present invention is human HG20, which was used in the present invention to construct a functional GABA-B receptor, for use in the method of the present invention.

Sequence 941 AA;

Query Match 15.9%; Score 1066.5; DB 22; Length 941;
Best Local Similarity 29.5%; Pred. No. 1.3e-85;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;

QY 155 LLGLFELSTSRGPRPDGLSELGAATMAVEHINRKRLLPGYTLLELVNTDTCDDPGVGVDRF 214

Db 58 imglptkavaksgigrvlpavelaieqirnesllrpyfldrlrlydtecdnakglkaf 117

QY 215 FHAIYQTPSTRMVMMLGSGACSEYTESLAKVVPYWNIVQVSFGSTSPALSRRPEPFYVRT 274

Db 118 ydaikygnp--hlmgvggpcsvtsiaeslqgnwlvlsfaattpvladkkyppffrt 175

QY 275 VAPDSSHNPARIATIRKFGGTVTTTSQNEEVHSLAVNNLVTELEAANISCAATITFA-- 332

Db 176 vpsdnavnpaillkllkhygkwrgvtltdqgrfsevrnditgvlgyedleisdtessnd 235

QY 333 -ATDFKEQLLLRETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391

Db 236 pctsavk----lkgndvriilqgfdqnaakvfccayeenmygskypwlpwyepswe 291

QY 392 DQRT-----ACSNHELQLAIVENLVVSTHNSIVGNVNSYGLNNHMFNSQLRKQSAQPHG 446

Db 292 qvhteanssrclrknlilaamegyi-----gvdfepilsskqiktsgktppqyer 340

QY 447 Q-DGFGSGYGPRIISAATQSDSRRRRRRGVCTSGHLFPPEAISQYAPQYDVAWAIALA 505

Db 341 eynnkrgvgp-----skfhgyaydgilwiakt 368

QY 506 LRAAEHWRNNEQSKLDGFDYTRSDMAWEFLQMGKHLHFLGVSGVPSFSGPDRVGTAF 565

Db 369 lgramethlhasrhqriqdfnydhtlgrilnamnetnfgvtgqvfvnrgermgtikf 428

QY 566 YQIQRGLEPVALYYPATDALDFRCPRCPVKWHSQVPTAKRVFKLURVATIAPLAFYTI 625


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Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;
QY 155 LLGLFELSTGRPRDGLSELGAATMAVEHINRRLKLLPGYTLELVNTDQCPGVGVDRF 214
Db 58 imglmpitkevaksigrvlpavelaleiqirnesllrpyfldrlrlytecndakglkaf 117
QY 215 FHAIYTOPSRWMLLGSACSEVTESLAKVVPYWNIVQVSTGSPALSDREFFYFRT 274
Db 118 ydaikygn--hlmvfgvcpvstilaeslqgnlvlsfaattpvladkkyppfrrt 175
QY 275 VAPDSSHNPARIAIRKFGWGTVTTFSEVHSLAVNLVTELEAANISCAATITFA-- 332
Db 176 vpsdnavnpaillkllkyqwrvtltdqvrfsevrndltgvygedleisdesfsnd 235
QY 333 -ATDFKOLLRLRETRRIIISGSQELAPQILCEAYRLRMFGADYAWILHESMGAPWMP 391
Db 236 pctsvek--lkgndvriilqgdqmaakvfccayeennmygskylipwyyepswwe 291
QY 392 DQRT-----ACSNHELQLAVENTLIVVSTHNSIVGNVNSYSLNNHMFNSQLRQSAQFHG 446
Db 292 qvhteansrcrlrknllaamegyi-----gvdfeplsskqiktsgktppqyver 340
QY 447 Q-DGFGSGYGPRIISAATQSDRRRRRGVGTSGHLFPPEAISQYAPQTYDAVNAIALA 505
Db 341 eynnkrgvgp-----skfhgdaydgiwviakt 368
QY 506 LRAAEHWRNREEQKLDGFDYTRSDMAWEFLQMGKHLFGVSGVPSFGPDVRGVTAF 565
Db 369 lqramethassrhrigqfndytdhtlgrilnametnffgtvgvfrngmgtklf 428
QY 566 YQIQGELLEVALYPATDALDFRCPRCPVPKWHSGQVPIAKRVFKLRVATIAPAFYFI 625
Db 429 tqfqsrevkvgynavadtleiind---tfrfgseppkdtiileqirkislpysil 485
QY 626 ATLSVGLAIAITLAFNLHRLKKAIKLSPKLSNIYAVGCFVYATVILLGLDHSITLP 685
Db 486 saltilgmimasaifnknrnlkikmspeymnnlilggmlsyasiflfgldgsfv- 544
QY 686 SAEDSFATVCTARVYLLSAGSLAFSGMFATYRVHRIFTRTGVSFKDKMLQDIOLILV 745
Db 545 -sektfctctvrtwiltvgtytafgamfaktwrhfaifknv--kmkkkilkdkilviv 601
QY 746 GGLLLVALLVTLNVVDPMERHNLHNLLETSATRSVYQVQVEVCRSQHTQTLWLVLY 805
Db 602 ggmlidcilicwqavdprrtvekysmepdpagdisirpllehcenhtwiliyiv 661
QY 806 AYKGLLLVGVYMAWETHVKKIPALNDSQYICVSVYSVVIITSAIVVVLNANLISERVTLAF 865
Db 662 aygllmlfgclawetrnvspalndskyagmsvynvgimcilgaavsfldrtdqpnvqf 721
QY 866 ITITALILTSTATLCFLFIPKLDIWARNDIIDPVIHSMGLKMECNTRFRVVDRELEQ 925
Db 722 civalvifcstlclvfpkl-----itlrtpdaatqnrfrq 761
QY 926 YRVEQNVYKKEIOALDAEIKRLERLESGLTFTTSTTT--SSSTSLITG-----GGHLKP 979
Db 762 f--tqng--kk-----edsktstsvtsvngqastsrleglsenhrilm 800
QY 980 ELT-----VTSGISOTPAASK-----NRTPSISG---ILPNLLIS 1011
Db 801 kiteldkdeventqlqdtpekttyikqnyhqelndilnlnfttestdggkailknhl-- 858
QY 1012 VLPPIVPRASWPSAE 1026
Db 859 ---dnpqlqwnnte 870
RESULT 7
AAW90938
ID AAW90938 standard; Protein; 941 AA.
XX
AC AAW90938;
XX
```

```
DT 14-JUL-2000 (first entry)
XX Human GABA-B receptor protein.
KW GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor;
KW human disease marker; gene therapy; central nervous system; epilepsy;
KW stroke; psychological disease; stress; manic depression; schizophrenia;
KW migraine.
OS Homo sapiens.
XX WO200015786-A1.
PN 23-MAR-2000.
XX 11-SEP-1999; 99WO-EP06742.
XX 14-SEP-1998; 98DE-1041941.
PR 04-DEC-1998; 98DE-1056066.
XX (BADI ) BASF-LYNX BIOSCIENCE AG.
XX Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;
XX WPI; 2000-283281/24.
XX N-PSDB; AAA11696.
XX A novel metabotropic receptor complex from the central nervous system,
XX related coding sequences and methods of identifying binding substances,
XX ligands and interactions with other proteins
XX Claim 5; Page 53-56; 66pp; German.
XX This invention describes a novel protein heteromer, containing at least
XX a GABA-B receptor protein and at least a protein (A) or a sequence which
XX has a substitution, inversion, insertion or deletion of one or more amino
XX acid residues and which retains the biological activity of the protein
XX heteromer and which has neuroprotective activity. The encoding nucleic
XX acid (I), the construct, (A) or the protein heteromer are useful for
XX identifying proteins (or nucleic acids encoding such proteins) that show
XX specific binding affinity to (A) or the protein heteromer. The two-hybrid
XX system or biochemical methods can be used to identify interaction domains
XX of metabotropic receptors and use for pharmacotherapeutic intervention.
XX Structural information from the protein or protein complex is useful for
XX identifying and manufacture of substances which have specific binding
XX activity to the protein or protein complex. The protein heteromer and
XX (A), or fragments of these are useful as antigens to generate specific
XX mono- or polyclonal antibodies. (I) is useful for identifying and
XX isolating homologous sequences, as a marker for human disease and for
XX gene therapy. The methods can be used to identify substances, which bind
XX to (A) or (I) and that cause inhibition or activation of functional
XX effects of the GABAergic signal messages in neurons of the central
XX nervous system. The method can also identify substances that inhibit or
XX amplify interactions of (A) with other metabotropic receptors or
XX interaction of ligands with the protein heteromer or (A) or interactions
XX of (A) with G-proteins or other signal transduction molecules. The
XX analysis of the interactions of (A) and GABA-B receptors is important
XX for identifying potential active substances against diseases such as
XX epilepsy, stroke and psychological diseases such as stress, manic
XX depression, schizophrenia, migraine and others. This sequence represents
XX the human GABA-B receptor described in the invention.
XX Sequence 941 AA;
```

```
Query Match 15.9%; Score 1066.5; DB 21; Length 941;
Best Local Similarity 29.5%; Pred. No. 1.3e-85;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;
QY 155 LLGLFELSTGRPRDGLSELGAATMAVEHINRRLKLLPGYTLELVNTDQCPGVGVDRF 214
Db 58 imglmpitkevaksigrvlpavelaleiqirnesllrpyfldrlrlytecndakglkaf 117
```


CC useful for treating drug addiction. Antagonists are used to treat
CC Alzheimer's disease. Functional assays were not possible with GABABR1
CC alone, so identification of a new GABABR2 polypeptide is useful for high
CC throughput screening assays for agonists or antagonists against GABAB
CC receptors using co-expression of GABABR1/R2. The pharmacological and
CC signal transduction properties of the two receptors GABABR1 and R2 match
CC those of native GABAB receptors in the brain.
XX
SQ Sequence 898 AA;

Query Match 16.0%; Score 1071.5; DB 20; Length 898;
Best Local Similarity 29.5%; Pred No. 4.3e-86;
Matches 271; Conservative 161; Mismatches 342; Indels 145; Gaps 20;

QY 151 GKIVLLGFLSTSRGPRDGLSELGAATMAVEHINRKLRLPGYTLLELVNTDQCDPGVG 210
DB 11 gplsmgmlptckevaksgirgvpavelaieqirnesllrpyfdlrlrlydtecdnag 70
QY 211 VDRFFHAIYTPQSTRMMLGACSEVTSIAKVPVWNIQVVSFSTSPALSDRRPEPY 270
DB 71 lkafydaikygnp--hlmwfgvcpsvtiaaelsqgwalvqisfaatpvladkkypy 128
QY 271 FVRTVPDSSHPARTAFTRKFGWGVTTFSONEEVHSLAVNVLVTELEAANISCAATIT 330
DB 129 ffrtvpssnavpalkllkhyqkrvgltqdvrfsevrndltgvlgedieisates 188
QY 331 FA---ATDFKEOLLRLRETDRIRIIGSFQSELAPOILCEAYRLRMFGADYAWILHESMGA 387
DB 189 fsndpctsvkk---lkgnvriilqgfdqgnmaakvfccayeenmygskyywiipgyep 244
QY 388 PWWPDQRT-----ACSNHELQIAVENLIVVTHNSIVGNVSYGLNHNMFNSOLRQKSA 442
DB 245 swveqhteansrclrnallaamegyi-----gvdfeplsskqiktisgktpq 293
QY 443 QFHGQ-DGFGSGYGPRIATAATQSDSRRRRRGVCTSGHLPPEALISOYAPOTYDAVWA 501
DB 294 qyereynkrsgvgp-----skfhgyaydgilw 321
QY 502 IALALRAAEHWRNEOSKLDGFDYTRSDMAWEFLQOMKGLHFLGVSPVSPGSDPRVG 561
DB 322 iaktlgramethasrhqridfydhtlgrliinamnetnffgvtgqvfvfngermg 381
QY 562 TTAIFYQIRGLLEVALYYPATDALDFRCPRCPVKNHSGQVPIAKRVKLRVATIAPLA 621
DB 382 tikftqgdsrevkgyevnavadtieind---tirfgseppkdktiileqirkislpl 438
QY 622 FYTATLSSVGTALAITFLAFNLHFRKKAIKLSSPKLSNITAVGCFYFVATVILLGLDH 681
DB 439 ysilisaltlilgmimasafllfnkqrnkqkikmsspymnnlililgmlsyasiflfgldg 498
QY 682 STLPSAEDSFATVCTARVYLLSAGSLAFSGFMFAKTYRVHRIFTRTGSVFKDKMLQDIOL 741
DB 499 sfv--sektfelctvrtwiltvgtytafgamfaktwrhaifknv--kmkxiikdql 554
QY 742 ILLVGLLLVDALVTLVWVTPDMERHLNLFLTEISATRSVVYQVQVEVCRSOHTQTWL 801
DB 555 lvivvgmllidcilicqavdplrttekysemepagdrisrpllehcenhtmtiwl 614
QY 802 SVLYAYKGLLVGVYMAWETHVKIPALNDQYICVSYVSVVITSIAVVVLANLISERV 861
DB 615 givvaykgllmlfgflawetrvnsipalndskygmsvynvgimcilgaavsfiltrdqp 674
QY 862 TLAFTITAILTSTATLCLLFIPKLHDIWARNDIIDPVIHSMGLKMECNTRRFVVD 921
DB 675 nvqfcivalviifsticilcvfpkl-----itlrtpdaatqn 714
QY 922 RELQYRVQNRVYKKEIQALDAIEIKRLERLESGLTTTSTTT---SSSTSLTGG---GG 975
DB 715 rrfqf---tqnq--kk-----edsktstsvtsvngqastsrleglsenh 753
QY 976 HLKPELT-----VTGISOTPAASK-----NRTPSISG---ILPN 1007
DB 1007

DB 754 rlrmkiteldkleevtmqldtpekttyikqnhqyelndilnlnftestdggkailkn 813
QY 1008 LLLSVLPVPIPRASWPSAE 1026
DB 814 hl-----dgnpqlqwntte 827
RESULT 4
AA70326
ID AAY70326 standard; Protein; 898 AA.
XX AC AAY70326;
XX DT 21-JUN-2000 (first entry)
XX DE Human gamma amino butyric acid receptor, GABA-B-R2 protein.
XX KW Gamma amino butyric acid; GABA-B-R2; human; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antisthmatic; antiaddictive;
KW uterine; analgesic; antitussive; agonist; neuroprotective; nootropic;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Domain 438..461
FT FT /label= Transmembrane_domain-I
FT Domain 475..501
FT FT /label= Transmembrane_domain-II
FT Domain 513..535
FT FT /label= Transmembrane_domain-III
FT Domain 554..576
FT FT /label= Transmembrane_domain-IV
FT Domain 612..634
FT FT /label= Transmembrane_domain-V
FT Domain 648..670
FT FT /label= Transmembrane_domain-VI
FT Domain 676..701
FT FT /label= Transmembrane_domain-VII
XX WO200012692-A1.
XX PD 09-MAR-2000.
XX PF 27-AUG-1999; 99WO-US19651.
XX PR 27-AUG-1998; 98US-0141760.
XX PR 16-OCT-1998; 98WO-US22033.
XX PR 04-NOV-1998; 98US-0186664.
XX PR 15-DEC-1998; 98US-0211755.
XX PA (SYNA-) SYNAPTIC PHARM CORP.
XX PI Jones KA, Laz TM, Borowsky B;
XX WPI; 2000-246751/21.
XX N-PSDB; AAZ51399.
XX PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
XX detecting receptor agonists useful for treating e.g. asthma,
XX incontinence, and Alzheimer's disease -
XX Claim 9; Fig 5; 260pp; English.
XX CC The present amino acid sequence is the human GABA (gamma amino butyric
XX acid)-B-R2 receptor protein isolated from human hippocampus cDNA library.
XX The coding region of GABA-B-R2 is cloned into the expression vector
XX pEXJ-HRT37 and the plasmid is designated as TL-267 (ATCC No. 203515).
XX GABA-B is a major inhibitory neurotransmitter, the receptors of which
XX are widely distributed throughout the central nervous system. GABA-B-R2
XX receptor has anticonvulsant, antisthmatic, uterine, analgesic,
XX antitussive, antiaddictive, nootropic and neuroprotective activity.

XX This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid-B (GABA-B) receptor which has insecticidal
CC activity. (II), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence represents a fruitfly (*Drosophila melanogaster*) GABA-B receptor
CC which is described in the method of the invention.

XX Sequence 1220 AA;

Query Match 18.3%; Score 1229; DB 22; Length 1220;
Best Local Similarity 30.5%; Pred. No. 6.2e-100;
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps 34;

QY 163 TSGRPDGLSELGAATMAVEHINRK-RLLPGYTLELVNTDQDGPVGVDYRFFHAIYQ 221
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 48 tgrgvmp-----svklalghvnehgkilanyrlhmwndtqnaavgvksffdmhmsg 100

QY 222 PSTRMVLLGSACSEYTESLAKVVPYNIQVSGSTSPALSDREPPFYFRTVAPDSSH 281
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 101 pn--kvmifgaacthvtdplakaskhwhltqlsyadthpmtf-kdafpofrrvpsenaf 157

QY 282 NPARIAFIRKFGTGVTFQSENEVHSLVNNLVTELEAANISCAATITFAATDFKEOLL 341
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 158 naprallkefntrvgtyvqnepryslphnmhvadidamevevetqsf-vndvaealk 216

QY 342 LIRETDTRIIGSFQELPAQILCEAYRLRMFGADYAWILHESMGAPWW-PDQRTACSNH 400
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 217 klrekdvriilgnfnehfarkafceaykldmygrayqlmatystdwnvtqdscevsve 276

QY 401 ELQAVENLIVSTHNSIVGNVSYGLNNHMF---NSQLR-KQSAQPHGQDQFGSGGTP 456
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 277 eiatalegailvdlplstsgditvagitadeyiveydrirgteysrfhg----- 326

QY 457 RISIAATQSDRRRRRGVGTSGGHLFPEAISQVAPOTYDAVVAIALALRAAAEEHWRN 516
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 327 -----tydgiwaalaiaqyvae----- 344

QY 517 EESQKLDGFDYTRSDMAWE--FLQMGKHLFLGVSGPVSFSGPDRVGTAFYQIQRLLE 574
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 345 kzedllthfdyrvkd--wesvflealntsfegvtgprfynnerkanilinqfqlgme 402

QY 575 PVALYPATDALDFRCPRCPVKHSGQVPIAKRVFKLRVATIAPLATYTTATLSSVGTIA 634
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 403 kigeyhsqkshldslg--kpvkwgvtppkdrtilylehsqvntliysasasvigi 460

QY 635 LAITELAFNLHFRKLKAIKLSPPKLSNITAVGCIFFVATVILLGLDHSFTLPSAEDSEATV 694
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 461 iatvflafnkynqrnykmsphnliivgcmitylsiflglid--ttlssvaafpyi 518

QY 695 CTARVYLLSAGFSLAFSGMFAKTYRVRIHFTRTGVSFVKDKMLQDILQLLGVGLLLVDAL 754
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 519 ctaravllmagflsfagmsktrvhsif--tdlknkvikdyqlfmvvgvllaiaida 576

QY 755 LVTLVWVTDPERH-----LHNUTLEISATDRSVVQPVQVECRSQHTQWLSVLYAYK 808
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 577 iittwgiadpfyretkqlplhnenid-----dvlvipeneycqhmtifvsiiaayk 630

QY 809 GLLLVGVYMAWETHRVKIPALNDSQYIGSVYSVITSVAIVVVLNLSERVTLAFITI 868
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 631 glllvfgafawethrvhsipalndsghifsvynvfitclagaaalslvsdrkdlvfvll 690

QY 869 TALILTSTTATLCLLFPKLDIARN--DIIDPVIHSMGLKMECNTRFRVVDERR--EL 924
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 691 sffifcttatclvfpkivel-kropqgvvdvrvtatlrpmkskngr--dsavcel 745

QY 925 QYRV-EVON---RYVK-----KEIQALDABIRKLERLLESGLTTTSTTSSTSLITGG 974
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :

Db 746 eqrlrdvkntrcfrkalmekenelqal---irklgpearkwidgvvtcggnsnv-----g 797

QY 975 GHUKP-----ELTVTSGISQTPAASKNRTPSISGILPNLLL 1010
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 798 selepilnddivrlsappvrrmpstvttemtsvdsthvmndn---sfvsqstvma 854

QY 1011 SVLPP-----VTPRASWPSAEYMQIPMRRSVT--FASQPOLEAEACILPAQDLINRLAHQ 1062
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 855 psippkklkqsivehshshapltmmqpiqqqlglqhgqmqgqhlqqgghqmqgqqq 914

QY 1063 QATEAKTGLINLRIGFIRTSSTNKGSTASLADQKG--LKAAPKSHMGLFTRLIPS-SQ 1118
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 915 qqqhhrhl--ekrnsvsaqddnigsitagkrsggdcsmrrrqstasrhydsq 972

QY 1119 TASCNAIYNPNODSIPSEASSHPNGNHLKPIHGRS---LTKSGTHLDH 1164
| | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
Db 973 tptarkpyssshrrnsstnistsqelsnmcphskpstpaviktptasdh 1021

RESULT 3
ID AAY14082
XX AAY14082 standard; Protein; 898 AA.
AC AAY14082;
XX
XX 20-JUL-1999 (first entry)
DE Human GABABR2 protein sequence.
DE
DE
KW GABABR2; gamma amino butyric acid class B receptor 2; spasticity; asthma;
KW incontinence; decreasing nociception; anti-tussive agent; drug addiction;
KW Alzheimer's disease; therapy.
XX
OS Homo sapiens.
XX
XX WO9920751-A1.
PN
PD 29-APR-1999.
XX
XX 16-OCT-1998; 98WO-US2202033.
PF
XX 27-AUG-1998; 98US-0141760.
PR 17-OCT-1997; 97US-0953277.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
PI Borowsky B, Jones KA, Laz TM;
XX
XX WPI; 1999-302737/25.
DR N-PSDB; AAX58005.
XX
XX Gamma amino butyric acid, class B, receptor 2 polypeptide and gene
PT sequences
XX
PS Claim 9; Fig 2a-d; 260pp; English.
XX
XX This sequence is the human gamma amino butyric acid, class B,
CC receptor 2 (GABABR2) polypeptide of the invention. The DNA can be used
CC for the production of GABABR2, and for the design of probes that are
CC useful for detection of the DNA or homologues in a sample. Antibodies
CC against GABABR2 are useful for detecting GABABR2 and GABABR1/R2 on the
CC surface of cells. Transgenic mice expressing GABABR1/R2 are useful for
CC determining the physiological effects of varying levels of the receptors
CC in the presence of an inducible promoter which regulates the receptors
CC expression. These transgenic mice can also be used to identify GABABR1/R2
CC antagonists or agonists that are capable of alleviating abnormalities
CC associated with the receptors. Recombinant cells expressing GABABR1/R2,
CC or membrane extracts from these cells, are useful for identifying
CC chemical compounds that specifically bind to the receptor. The cells can
CC also be used to determine whether the chemical compounds are antagonists,
CC agonists, activators or inhibitors. Agonists of GABABR1/R2 are useful for
CC treating spasticity, asthma, incontinence and decreasing nociception. The
CC agonists can also be used as anti-tussive agents. Agonists are also

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XX Claim 2; Page 51-59; 62pp; German.
PS
XX This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I)
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor
CC which is described in the method of the invention.
XX
SQ Sequence 1305 AA;
    Query Match      100.0%; Score 6705; DB 22; Length 1305;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Y 1 MRIIPVQGTGRYPMPAVGLRLVLALAWATSAAMMESSAELQALGHEAIRPGAASTIS 60
    D 1 mriipvgqgtrygpavglrlvlalawatsaaamesaelqalghairpgaaasists 60
    Y 61 SPSSPPGESASTVTAGTPIPPRSQWKYKRYKVRQRLNLSHNLPGSTNASHAHLL 120
    D 61 spssppgesastvtagtpiprrsqwkrykrykvrqrlnlsnlpgstnashahll 120
    Y 121 NUPPQRQLKVNQVFERMRSPAEQNRHKGITVLGLFELSTSRGPRPDGLSELGAATM 180
    D 121 nuppqrylkvnqvfermrspaemqrnkgitvlglfelstsrgrpdpdglseigaatm 180
    Y 181 AVEHINRKLPGYTLELVNTDTCQDPGVGVDRFFHAIYTPQSTRMVLGSAACSEYTES 240
    D 181 avehinrklpgytlevntdqdpvgvdrffhaiytpqstrmvlmgacsceytes 240
    Y 241 LAKVVPYNIVQVSGTSPALSDRREFFYFYTVPADPSHNPARIATIRKFGWGTTF 300
    D 241 lakvvpynivqvsfgstspalsdrrefyfytvpadsnmpariafirkfgwgttff 300
    Y 301 SONEEVHSLAVNVLTELEAANISCAATITFAATDFKEQLLLRETTTRIIIGSFQOLA 360
    D 301 sneeevhs lavnvlteleaaniscaatitfaatdfkeqlllrettriiigsfsgela 360
    Y 361 PQILCEAYRLRMFGADYAWILHESMGAPWMPDQRTACSNHELQALAVENLIVVSTHNSIVG 420
    D 361 pqilceayrlrmfgadyawilhesmgapwmpdqrtacsnhelqlavenlivvsthnsivg 420
    Y 421 NNVSYSGLNNHMFNSQLRKQSAFHQDQFGSGYGPRIISIAATQSDSRRRRRRGVGTSG 480
    D 421 nnvsysglnnhmfnsqlrkqsafhqdgqfsgsgygpriisiaatqsdrrrrrgvgtsg 480
    Y 481 GHLFPEATISOYAPQYDAWATALARAEEHWRNEEQSKLDGFDYTRSDMAWEFLQOM 540
    D 481 ghlfpeaisqyapqydaawatalaraeehwrneeqskldgfdytrsdmaweflqom 540
    Y 541 GKLHFLGVSGPVSFSGPDRVGTAFYQIQRGLEPVALYPPATDADLDFRCPRCPVKWHS 600
    D 541 gklhflgvsgpvsfsgpdrvgtafyqiqrglepvallyppatdaldfrpcrcprvkwhs 600
    Y 601 GOVPIAKRVFKLRVATPIAPFYTIATLSSVGIATLAFNLHFRKKAIAKLSSPKLS 660
    D 601 govpiakrvfkrlrvatpiapfytiatlssvgialaitflafnlhfrkkaiklsspkls 660
    Y 661 NITAVGCCIFVYATVILLGLDHTLSAEDSPATVCTARVYLLSAGFSLAPGSMFATYRV 720
    D 661 nitavgcifvyatvillglldhtlsaedspatvctarvyllsagfslapgsmfatyrv 720
    Y 721 HRIFRTGSVFKDKMLQDILQLILLVGLLLVDALLVTLVAVTDPMERHLNLTLEISATD 780
    D 721 hrifrtgsvfkdkmlqdiqlillvglldvallyvttlvdpmmerhlnltleisatd 780

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QY 781 RSVVYQVEVCRSOHTOTWLSVLYAYKGLLVGVYMAWETRHVKIPALNDSOYIGVSV 840
DB 781 rsvvyqpvevcrshtotwlsvlyaykglilvvgvymawetrhvkpainsdqyigvsv 840
QY 841 YSVVITSIVVLANLISERVTLAFITITALTSTTATCLLFLPKLHDHWARDIIDP 900
DB 841 ysvvitsaivvvanliservtlafititaltsttatlcllfpklhdiwardiidp 900
QY 901 VIHSMGLKMECNTRFRVDDRELQYRVQNRVYKKEIQALDAEIRKLERLLESLGTTT 960
DB 901 vihsmglkmecontrfrvddrelqyrvqnrvykkeiqaldaeirklerllesglttt 960
QY 961 STTSSSTSLTGGHLKPELTVTSGISOTPAASKNRPSISGILPNLLSVLPVPIRA 1020
DB 961 sttssstsltggghlkpeltvtsgisotpaasknrpsisgilpnllsvlpvpvira 1020
QY 1021 SWPSAEYQIWMRRSVTFASQPOLFEACLPADQLINLRLAHQOQAEAKTGLINRLRGIFS 1080
DB 1021 swpsaeymqipmrrsvtfasqpoleeaclpadqlinlrlahqgateaktglinrlrgifs 1080
QY 1081 RTTSSNKGSTASLADQKGLKAAFKASHMGLFTRLIPSSOTASCNAINYNPNQDSIPSEASS 1140
DB 1081 rttssnkgstasladqkglkaafkashmglftrlipssqtascnainynpnqdsipseass 1140
QY 1141 HPNGNHLKPIHRGSLTKSGTHLDHLTKDPNPLPIPTISGGEQDQTLGGKYVKLLETKNV 1200
DB 1141 hpngnhlkpihrsgltsksthldhltdkpnplpiptisggedqdtlggkyvklletkvn 1200
QY 1201 FOLPSNRPPSVVQPPSLRVRGSPRPRLPTPTCSLSALAESEDRPGDSTSLGSK 1260
DB 1201 folpsnrppsvvqppslrvrgsprprhlptptcslsalaeasedrpgdstslgsk 1260
QY 1261 SIPRISLQOVTSGGTWKSMETVGSRLSLGDSQEEQOAPANGTE 1305
DB 1261 siprlsqvtsggtwksmetvgksrlslgdsqeeeqapangte 1305
RESULT 2
AAB86160
ID AAB86160 standard; Protein; 1220 AA.
XX
AC AAB86160;
XX
XX 03-AUG-2001 (first entry)
XX
DE D. melanogaster GABA-B receptor protein SEQ ID 4.
XX
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect.
XX
OS Drosophila melanogaster.
XX
PN DE19955408-A1.
XX
PD 23-MAY-2001.
XX
XX 18-NOV-1999; 99DE-1055408.
XX
XX 18-NOV-1999; 99DE-1055408.
XX
XX (FARB ) BAYER AG.
XX
XX Raming K, Mezler M, Mueller T;
XX
XX WFI; 2001-318282/34.
XX
XX N-PSDB; AAH20520.
XX
XX New invertebrate gamma-aminobutyric acid receptor proteins, useful in
XX screening for potential insecticides, for plant protection or medicine,
XX also related nucleic acid
XX
XX Claim 2; Page 32-39; 62pp; German.

```

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:00:32 ; Search time 52.81 Seconds
(without alignments)
1830.442 Million cell updates/sec

Title: US-09-715-962-6

Perfect score: 6705

Sequence: 1 MRIIPVQTRYGPWPVGL.....RLSLGDSQEEQQAPANGTE 1305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

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4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6705	100.0	1305	22 AAB86161	D. melanogaster GA
2	1229	18.3	1220	22 AAB86160	D. melanogaster GA
3	1071.5	16.0	898	20 AAY14082	Human GABABR2 prot
4	1071.5	16.0	898	21 AAY70326	Human gamma amino
5	1069.5	16.0	940	21 AAY44343	Rat gb2 GABA B rec
6	1066.5	15.9	941	20 AAY29796	Human gamma-amino-
7	1066.5	15.9	941	21 AAY90938	Human GABA-B recep
8	1066.5	15.9	941	21 AAY51928	Human GABA-B recep
9	1066.5	15.9	941	21 AAY70328	Human GABA-B-R2 re
10	1066.5	15.9	941	21 AAY79202	Human GABAB recept
11	1066.5	15.9	941	21 AAY44342	Human gb2 GABA B r

12	1066.5	15.9	941	22 AAB50088	HG20 protein seque
13	1066.5	15.9	943	20 AAY28837	Human GABABR2 rece
14	1065.5	15.9	940	21 AAW90937	Rat GABA-B recepto
15	1065.5	15.9	940	21 AAY70327	Rat gamma amino bu
16	1065.5	15.9	1303	20 AAY49132	GABA-BR2*Gqo5 fusi
17	1064.5	15.9	940	21 AAY51927	Rat GABA-B recepto
18	1058.5	15.8	883	20 AAY14081	Rat GABABR2 protei
19	1058.5	15.8	941	21 AAY68743	A human gamma-amin
20	1058	15.7	914	21 AAY44344	Protein-1 related
21	1055	15.7	965	21 AAY44345	Protein-2 related
22	1018.5	15.2	840	22 AAB86159	D. melanogaster GA
23	994	14.8	844	19 AAW40118	Rat GABA-BR1b rece
24	994	14.8	844	19 AAW40119	Human GABA-BR1b re
25	994	14.8	844	20 AAY28839	Human GABABR1b rec
26	994	14.8	844	20 AAY14102	Human GABAB recept
27	994	14.8	844	21 AAY32467	Human G-protein Co
28	992.5	14.8	960	19 AAW40116	Rat GABA-BR1a rece
29	992.5	14.8	961	20 AAY29798	Human gamma-amino-
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32	991.5	14.8	960	21 AAY83145	Human GABAB1A rec
33	991.5	14.8	961	20 AAY28838	Human GABAB1A rec
34	991.5	14.8	961	20 AAY14101	Human GABAB recept
35	991.5	14.8	1323	20 AAY49133	GABA-BR1a*Gqo5 fus
36	990.5	14.8	960	20 AAY28841	Human GABAB1A rec
37	990.5	14.8	960	20 AAY49122	Rat GABABR1a rece
38	989.5	14.8	960	20 AAY29797	Murine gamma-amino
39	988.5	14.7	899	20 AAY14107	Human GABAB recept
40	987.5	14.7	960	22 AAB50089	Murine GABA-B-R1a.
41	984	14.7	892	20 AAY14109	Human GABAB recept
42	982	14.6	962	22 AAB50090	Human GABA-B-R1a.
43	979.5	14.6	793	19 AAW40117	Human GABA-BR1a/b
44	976	14.6	859	20 AAY34111	Human GABA recepto
45	976	14.6	859	20 AAY30311	Amino acid sequenc

ALIGNMENTS

RESULT 1
ID AAB86161 standard; Protein; 1305 AA.
XX AAB86161;
AC
DT
DT 03-AUG-2001 (first entry)
XX
DE D. melanogaster GABA-B receptor protein SEQ ID 6.
XX
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect.
XX
OS Drosophila melanogaster.
XX
PN DE19955408-A1.
XX
PD 23-MAY-2001.
XX
PF 18-NOV-1999; 99DE-1055408.
XX
PR 18-NOV-1999; 99DE-1055408.
XX
PA (FARB) BAYER AG.
XX
PI Raming K, Mezler M, Mueller T;
XX
DR WPI: 2001-318282/34.
DR N-PSDB; AAH20521.
XX
PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in
PT screening for potential insecticides, for plant protection or medicine,
PT also related nucleic acid

258	Db	RPGEFEKIIIRLLETPNARAVIMFANEDDTRRILEAKKLUNQSG-HFLWIGDSWGSKIA	316
388	Qy	PWPDQRTACSNHELQLAVENTLIVSTHNSIVGNVNSYGLNNH-----MFNSQLRKQSA	442
317	Db	PVYQOEIEA-----EGAV-----TILPKRASIDGDFRYFSRRTLANNRRNVFA	360
443	Qy	QFHQDQFG--SGYGRPISIATQSDSRRRRRRGVGTSGGHLFPFAISQVAPQYDVA	499
361	Db	EF-WEENFGCKLAGSHGRNRIKCTGLERAIARDSVSEQEGKVOF-----VIDAV	409
500	Qy	WAIALALRAAEEHWRNE-----EQSKLDGFDYTRSDMAWEFLQOMKGLHFLGVS	549
410	Db	YSMAYAL-----NMHKDLCPYIGLCPRMSTIDG-----KELGYIRAVINFGSA	455
550	Qy	G-PVSFS-GPDRVGTTFAYQIQ-----RGLEPPVAL	578
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579	Qy	-----YYPATDALDFRCPRC-----RP-----	595
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596	Qy	---VKWHS--GOYPIAKRVFKLVAITAPLAFTIATLSVGTALAITFLAENLHFKLK	650
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613	Db	IVRASGRELSVLLTGIFLCYSITFL-----MIAAPDTI--ICSFRRVFLGLGMCFSY	663
711	Qy	GSMFAKTRYVHRIFTR-TGSVFKDKMLQDITQLILLGGLLDALLVTLWVYTD-----	764
664	Db	AALLTKNRIHRIFEQCKSVTAPKFPISAPQSLVITFSLISVOLLGVFWFVVDPPHII	723
765	Qy	-----MERHLNHLFLEISATORSVVYQPOVEVCRSQHTQWLSVLYAYKGLLLVGVY	817
724	Db	DYGEQRTLDPEKARGVULKDISLSL-----ICS-----LGSYILLMVTCTV	765
818	Qy	MAWETRVKIPALNDSQYIGCVSVSV-VITSATVVVYLANLI--SERVTLAFITITALIIT	874
766	Db	YANKTRGP-ETNEAKPIGFTMITTCIIWLAFIPFPGTAQSAEKMYIOTTTLTVSMSL	824
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Search completed: April 30, 2002, 10:05:11
Job time: 789 sec

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; LENGTH: 867
; TYPE: prt
; ORGANISM: Homo sapiens
US-08-617-785-4
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Query Match	5.1k; Score 339; DB 4; Length 867;
Best Local Similarity	19.2k; Pred. No. 3e-21;
Matches 195; Conservative 163; Mismatches 367; Indels 290; Gaps 39;	
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Qy 248 WNIQVQSGSTSPALSDRREPPYFYRTVADSSHNPARIAIRKPGWGTVTTFSSONEVH 307	
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Qy 308 SLAVNNLVTELEAANISCAATITPAATOKBOLL-----LLRETTRIIGSFSOEL 359	
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Db 289 -----EGFDAYFTSRTLENNRRNNWFAYEENFNCKLTISGSKKEDTDRKCTG----- 337	
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Db 389 GG-----KLLKYIRNNVFNNGSAGTVPYMFNKGNDGAPGRYDIFQYTTNSPGYRL 439	
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Qy 756 VTLVWVTDPMERHLNHLFLEISATDRSVVYQDQVE--VCRSOHTQTLWSLVLYAYKGLLV 813	
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QY 991 PAASKN--RTPSTGILPNLLSVLPVPRASWPSEAEMQIPMRRSVTFA SQP 1042
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RESULT 15

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US-08-855-146-2
; Sequence 2, Application US/08855146
; Patent No. 6221609
; GENERAL INFORMATION:
; APPLICANT: Belagaje, Rama M.
; APPLICANT: Wu, Su
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Department
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,146
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,243
; FILING DATE: 07-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-10836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-63334
; TELEFAX: (317)276-2764
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-855-146-2

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Best Local Similarity 20.7%; Pred. No. 5.5e-21;
Matches 207; Conservative 133; Mismatches 339; Indels 301; Gaps 45;

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Db	139	PFTKPD-KISGVIGAAASSIVMANNILRLFKIPQISYASTAPELSDNTRYOFFSRVVP	197
Qy	277	PDSSHNPIARIAPIRKFGMGTVTTFSQN---EEVHSLAVNNLVLEAANISCAATITFAA	333
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Qy	334	T--DFKEQLLLRLT-DPRTIIGSFQSOELAPOILCEAYRLRMFGADYAWILLHESMG---A	387

QY 809 GLLLVGVYMAWETRVHKIPA-LNDSOYIGVSVSVVITSVAIVVLANLISERVTLAFIT 867
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QY 868 ITALILTST-----TATLCL-----LFIPLKLDI 891
Db 779 I--FYVTSSDYRVQTTMCVSVLSGVSVLGCLFAPKLHII 817
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US-09-258-523-2
; Sequence 2, Application US/09258523
; Patent No. 6103475
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/258,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/337,797
; FILING DATE: No. 6103475ember 14, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9431
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 872 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-258-523-2

Query Match 5.1%; Score 340.5; DB 3; Length 872;
Best Local Similarity 21.7%; Pred. No. 2.2e-21;
Matches 191; Conservative 113; Mismatches 344; Indels 233; Gaps 35;
QY 151 GKVLGLFELSTSRGPRPD-----GLSELGAATMAVEHINR-KRLLPG----- 193
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QY 194 -----YTELVTNDTCDDPGVGVDRFPH-----AIYQSTRMVLMLGSGACSEVTE 239
Db 90 DSCSKDTHALEQALDVRASLSRAGSGSRHICPDGSGYATHGDAPTAITGVIGSGYSVSI 149
QY 240 SLAKVVPYNNIVQVSGSPALSDREPPFYRTVAPDSSHNPARIATFKFCGCTVTT 299
Db 150 QVANLLRLFOIQIISYASTSAKLSDRSYDIFARTVPPDFEQAKAMAEILLRFNWTYVST 209

QY 300 FSONEEVHSLAVNNLVTELEAANISCAATI-----TFAATDFKEOL-LLLRDTDTRIIG 353
Db 210 VASEGDYGETGLEAELEARARNI-CVATSEKVGGRAMSRAAFEGVVVRAULLQKPSARVAVL 268
QY 354 SFSQELAPQIILCEAYRLRMFGADYAWILHESMGA----- 387
Db 269 FTRSEDARELLAASORL---NASFTWASDGGWGALESVVAGSEGAEGAITIELASYPIIS 325
QY 388 -----PW-----WPDQRTACSNHEILQLAVERNLIIV----- 412
Db 326 DFASYFQSLDPWNNSRNPWFREFW-EQRFRCFSFRQDCAHSLRAVVPFQESKIMFVVNA 384
QY 413 -----STHNSIVGNVNSYSGLNHMFNSQLRKSQAQFHGQDGFSGSGYCPRIISIAAT 463
Db 385 VYAMAHALHNMHRLALCPNTRLCDAMPVNGRRLLYK---DFVLNVKFDAPFRP---ADT 437
QY 464 QSDSRRRRRGVGTSGGHLFPPEAISQAPQYDAVMAIALALRAAEHWRNEEQSKLD 523
Db 438 HNEVRFDR-----FGDGIGRYNIFTY-----LRAGSGRYRYQKVGYNWAE 476
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Db 630 -GVCALERLGVGTAFSVCYSALLTKTNRITAFGGAREGAQ-RPRFISPASVAICLALI 687
QY 750 LVDALLVTLVVYDPMERHLNHLTLEISATDRSVV-YOPQVEVCRSQHTQTWLSVLYAYK 808
Db 688 SGQLLIVVAVLV-----VEAPGTGKETAPERREVVTLCNHRDASMLGSLAYN 735
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QY 868 ITALILTST-----TATLCL-----LFIPLKLDI 891
Db 779 I--FYVTSSDYRVQTTMCVSVLSGVSVLGCLFAPKLHII 817
RESULT 14
US-08-617-785-4
; Sequence 4, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810666.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

Db 215 ALKNYVSTVASEGSGVEAFIQKSDRGVCIAQSVKIPREPKAGEFDKIIRLLE 274
QY 346 TDTRIIIGSFQELAPQILCEYRLRMFGADYANILHESMGAPWMDORTACSNHQLQA 405
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QY 406 VENLIVVSTHNSIVGNVSYSG--LNNHMFNSQLKQSAQFHGQDGFSGYGPRIISAAT 463
Db 329 EGAVTILPKRMSVRGDFRYSRTLDNNRNITWF-----AEF-WEDNFHC-----KLSRHAL 379
QY 464 QSDRRRR--RRGVVGTSGGHLFPEAISQYAPQTDVAVMAIALALRAAEHW--RRNEEQ 519
Db 380 KKGSHVKKCTNRERIGQDSAY-EQEGKVQF---VIDAVYAMGHALHMRDLCPRGVGLC 435
QY 520 SKLDGFYTRSDMAWEFLQMGKHLFLGVSG-PVSFS-GPDVRGTTAFYQIO----- 569
Db 436 PRMDPVDT-----QLLKYIRNVFSGIAGNPVTFNENGADAPGRYDIYQYQLRNDSAEY 489
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Db 600 AATFLVWITFVRYN---DTPIVKASGRELSVLLAGIFLCYATTFPLM-----IAEP 647
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Db 707 ISQLLGLGVWFVDP-----SHSVVDFQDQRTLDPFRFARGVLKDCISDL 751
QY 800 WLSVLYAKGLLVGVYMAWETHRVKIPALNDSQYIGVYSV-VITSAIVVL--ANL 856
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Db 811 SADKLYIQTTTLTVSVLSASVSLGLMXPVYII 845

RESULT 12

US-08-337-797A-2
; Sequence 2, Application US/08337797A
; Patent No. 6017697
; GENERAL INFORMATION:
; APPLICANT: Burnett, J. P.
; APPLICANT: Mayne, Nancy G.
; APPLICANT: Sharp, Robert L.
; APPLICANT: Snyder, Yvonne M.
; TITLE OF INVENTION: EXCITATORY AMINO ACID RECEPTOR PROTEIN
; TITLE OF INVENTION: AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337,797A

; FILING DATE: No. 6017697ember 14, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9431
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 872 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-337-797A-2

Query Match 5.1%; Score 340.5; DB 3; Length 872;
Best Local Similarity 21.7%; Pred. No. 2.2e-21;
Matches 191; Conservative 113; Mismatches 344; Indels 233; Gaps 35;
QY 151 GKIVLLGLFELSTSRGPRD-----GLSELGAATWAVEHINR-KRLLPG----- 193
Db 30 GDLVLGLFPVHQKGPAEDCGPVNEHRGIQRLLEAMLFALDRINRDHPHLLPGLRGAIL 89
QY 194 -----YTLELVNTDQCQDGVGVDRFFH-----AIYQPSRTRMVMLLGSACSEVTE 239
Db 90 DCSKDHAEALDQALDFVRASLSRGADGSRHICPDGSAATHGADGAPTAITGVIGGSYSDVSI 149
QY 240 SLAKVPYWNIVQVSGFSTSPALSDRRFPFYRTVPDSSHNPARIARFKFGMGTVTT 299
Db 150 QVANLLRLFPQISYASTSAKLSKRYDYFARTVPDPDFQAKAMAEILRFFNNYVYST 209
QY 300 FSQNEEVHSLAVNNLVTELEAANISCAATI-----TPAATDFKEOL-LLLRETDRIIG 353
Db 210 VASEGDYGETGIEAFELEEARANI-CVATSEKVRAMRAAFEGVVRALLOKPSARVAVL 268
QY 354 SFSQELAPQILCEAYRLRMFGADYANILHESMGA----- 387
Db 269 FTRSEDARELLAASQRL---NASFTWASDQWGALESVAVSGEAGAEITELASYPIS 325
QY 388 -----PW-----WPDQRTACSNHQLQALAVENLIV----- 412
Db 326 DFASYFQSLDPWNSRNPNWFREFW-EQRFCSFRQDCAHSLRAVPPEQESKIMFVNA 384
QY 413 -----STHNSIVGNVSYSGLNHMFNSQLKQSAQFHGQDGFSGYGPRIISAAT 463
Db 385 VYAMAHALHNMHRALCPNTTTLCDAMRPVNGRRLYK---DFVLNVKFDAPFRP-----ADT 437
QY 464 QSDRRRRRGVVGTSGGHLFPEAISQYAPQTDVAVMAIALALRAAEHWRNEEQSKLD 523
Db 438 HNEVRFDR-----FGDGIGRYNIETY-----LRAGSGRYRQKVGYWA 476
QY 524 GFDYTRSDMAWEFLQMGKHLFLGVSGPVSPFSG-----PDRVGTAFYQIQRLLEPVA 577
Db 477 GLTLDTSLIPWASPS-----AGPLPASRSEPCQLQNEVKSVQPGVCCWLCIPQ 526
QY 578 LYYPATDALDFRCPCRCRPVKWH-----SQVPIAKRVFKLRVA-TIAPLAFYTIATLSSVG 632
Db 527 PYEYRLD--EFTCADCGIGYWPNASLTCFELPOEYIRMGDAWAGPV---TIACLG--- 578
QY 633 IALAITF-LAFNLHFRKKAIKLSSPKLSNITAVGCIFFVATVILLGLDHSPLSAEDSF 691
Db 579 -ALATFLVILGVFVRHNATPVVKASGRELCYILGCVFLCYCMFTFIAKPST----- 629
QY 692 ATVCTARVILLSAGSLAFSGMFAKYRVHRIF--TRTGSVFKDKMLQDIQILILVGLL 749
Db 630 -GVCAIRRLGVGTAFSVCSYALLTKNRIARIFGGAREGAQ-RPRFISPASQVAICLAI 687
QY 750 LVDALLVTLWVTDPMERHLNHLTLEISATRSVV-YOQOVECRSQHTQTWLSVLYAYK 808
Db 688 SGOLLIVVAVLV-----VEAPGTGKETAPERREVVTLCNRHDSMGLSLAYN 735


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Db 382 KKEDTRKCTG-----QERIGKDSNYEQEGKQVQFVIDAVYAMAHAL-----HHMNK 427
QY 516 N-----EQSKLDGDFYTRSDMAWEFLQOMKHLFLGVSG-PVSFS-CPDRVGTGA 564
Db 428 DLADYRGVCPMEQAGG-----KKLLKYIRHVNFGSAGTPVMENKNDAPGRYD 478
QY 565 FYQIQ-----RGL-----572
Db 479 IFQYQTTNTTNGYRLIGOWTDELQNLNEDMQWKGKGVREIPSSVCTLPCKPQORRKTQK 538
QY 573 -----LEPVALYYPATDALDFRCPRC---RPVKWHS--QVPIAKRVFKLRVATIAPL 620
Db 539 TPCWTCPCDGYQYQFD--EMTQCHCPYDQRPNENRTGCGQNIPIKLEWHSWAVIP--594
QY 621 AFYTIATLSSVGIATLITFLAFNLHFRKKAIKLSSPKLSNITAVGCFIVYATVILLGLD 680
Db 595 -----VFLAMGLGIATIFVMATFIRYNDTPIVRASGRELVSLLGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFGSMFAKTYRVHRIETR-TGSVEFKDKMLQDI 739
Db 647 -----IAKPDVA-VCSFRRVFLGCMCISYAALLTKNRIYRIFEQGKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLVVTDPMERHLNLTLEISATDRSVVYQOQVE--VCRSQHT 797
Db 701 SQAITSLSISVQLLGVFIWFGVDP-----PNIIDY---DEHKTMPNEQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRHVKIPALNDSQYIGVSVSV-VITSALVVVLANL 856
Db 753 DLQIICSLGYSILLMVTCTVYAIKTRGVP-ENFNEAKPIGFTMYTTCIVWLAFIPFFGT 811
QY 857 I--SERVTLAFITITLITLTSTTATLCLLPKLDHI 891
Db 812 AQSAEKLYIQTTLTITISWNLSSASVALGMLYMPKVYII 848

RESULT 9
US-08-176-401B-2
; Sequence 2, Application US/08176401B
; Patent No. 6274330
; GENERAL INFORMATION:
; APPLICANT: Segerson, Thomas P.
; APPLICANT: Kinzie, J. Mark
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Saugstad, Julie A.
; APPLICANT: Westbrook, Gary L.
; TITLE OF INVENTION: L-AP4 SENSITIVE GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.401B
; FILING DATE: 30-DECEMBER-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-176-401B-2

Query Match 5.2%; Score 348.5; DB 4; Length 915;
Best Local Similarity 20.4%; Pred. No. 4.6e-22;
Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;

QY 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSELGAATMAVEHINR-KRLIPGYTL- 196
Db 44 RIECDVTGLGLFPVH-AKGPSGVPCGDIKRENGIHRLEAMLYALDQNSDNLPLPNVTLG 102
QY 197 -----ELVTDNTOCDPGVGVDREFFHAIYTOPSTRMVMILG 231
Db 103 ARILDTCSTRTYALEQSLTFVQALIQDTSVRCNGB-----PPVFVKPE-KVGVIG 155
QY 232 SACSEVTESLAKVVPYWNIVQVSFGSTSPALSDRREEPYFYRTVAPDSSHNPARIATIRK 291
Db 156 ASGSSVSIMVANILRLFPQIPQISYASTAPELSDDRYDFFSRVVPPDSFOQAAMVDIVKA 215
QY 292 FGMGTVTTFQNEEVHSLAVNNLVTELEAANISCAAITFAATDFKEOLL-----LL 343
Db 216 LGWNYVSTLASEGSGYGEKGVSEFTQISKEAGGLCIAQSVRIPOERKORTIDFRIIKQL 275
QY 344 RETDTRIIGSFQELAPQILCEAYRLRMFCADYAWILHESMGAPWMPDQRTACSNHELQ 403
Db 276 DTNSRAVWTFANDEDIKQILAAAKRADQV--HFLWGSDSWGSKINP-----LHOHE 327
QY 404 LAVENLIVSTHNSIVGNVNSYSGLNHMFNSQLRKQSAQPHGQDGFSGSGYGPRIATAAT 463
Db 328 DIAEGAITIQPKRATV-----EGFDAYFTSRTLENNRRNVWFAEYEEENCKLTISGS 381
QY 464 QSDSRRRRRGVCTSGGHLFPEAI---SQYAPO-----TYDAVATAALARAEEHWR 515
Db 382 KKEDTRKCTG-----QERIGKDSNYEQEGKQVQFVIDAVYAMAHAL-----HHMNK 427
QY 516 N-----EQSKLDGDFYTRSDMAWEFLQOMKHLFLGVSG-PVSFS-CPDRVGTGA 564
Db 428 DLADYRGVCPMEQAGG-----KKLLKYIRHVNFGSAGTPVMENKNDAPGRYD 478
QY 565 FYQIQ-----RGL-----572
Db 479 IFQYQTTNTTNGYRLIGOWTDELQNLNEDMQWKGKGVREIPSSVCTLPCKPQORRKTQK 538
QY 573 -----LEPVALYYPATDALDFRCPRC---RPVKWHS--QVPIAKRVFKLRVATIAPL 620
Db 539 TPCWTCPCDGYQYQFD--EMTQCHCPYDQRPNENRTGCGQNIPIKLEWHSWAVIP--594
QY 621 AFYTIATLSSVGIATLITFLAFNLHFRKKAIKLSSPKLSNITAVGCFIVYATVILLGLD 680
Db 595 -----VFLAMGLGIATIFVMATFIRYNDTPIVRASGRELVSLLGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAFGSMFAKTYRVHRIETR-TGSVEFKDKMLQDI 739
Db 647 -----IAKPDVA-VCSFRRVFLGCMCISYAALLTKNRIYRIFEQGKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLVVTDPMERHLNLTLEISATDRSVVYQOQVE--VCRSQHT 797
Db 701 SQAITSLSISVQLLGVFIWFGVDP-----PNIIDY---DEHKTMPNEQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRHVKIPALNDSQYIGVSVSV-VITSALVVVLANL 856
Db 753 DLQIICSLGYSILLMVTCTVYAIKTRGVP-ENFNEAKPIGFTMYTTCIVWLAFIPFFGT 811
QY 857 I--SERVTLAFITITLITLTSTTATLCLLPKLDHI 891
Db 812 AQSAEKLYIQTTLTITISWNLSSASVALGMLYMPKVYII 848

RESULT 10
PCT-US94-14989-2
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Db 216 VSTLASEGNGESVFAFVQISREAGGVCIAQSIKIPREKPGFEFSKVIIRLMETPNARG 275
QY 352 IGFSQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHEHLQLAVENTIV 411
Db 276 IIFANEDDIRRLEAARQANLTGHFLWVGSDSWGAKTSP-----ILSLEDVAV 324
QY 412 VSTHNSIVGNVSYSGLNHMFNSQLKQSAQFHGQDGFSGYCPRIASIAATQSDSRRR 471
Db 325 GAI--TILPKRASIDGFDQYFMTSRLENNRNINWFAEFNEFNCKLTSGTQSDSDTRK 382
QY 472 RRGVGTSGGHLFPEAISVAPOTY-----DAVMAIALARAAEE-----HWRN 516
Db 383 CTG-----EERIGR--DSTYEQEGKVQFVIDAVYALAHALHSHQALCPGHGILC 430
QY 517 EQSKLDGFDYTRSDMAWEFLQMGKHLFLGVSG-PVSFS-GPDVGTGTAIFYQIQ----- 569
Db 431 PAMEPTDG-----RMLQYIRAVRENGSAGTPVMFNENGDPAGRYDIFOYQATNGS 481
QY 570 -----RGLLEPVALY 579
Db 482 ASSGGYQAVGQWAEIIRLDVEALQWSDPHEVPSLGLPCGPGGERKKMKGV--PCWH 539
QY 580 YPATDAL-----DFRCPRC---RPVKWHSQVPIAKRVEKLRVATIAPLAFYTIATLSS 630
Db 540 CERACDGRFOVDETCACPDGMRPTNHTGCRTP-----VVRUSWSPWAAPPL-LLAV 594
QY 631 VGIALATFLAFNLHFRKRLKAIKLSPPKLSNITAVGCFIVYATVILGLDHSHTLPSAEDS 690
Db 595 LGIVATTVVATVRYNNTPIVRASGRKLVLLTGIFLIYAITFLM-----VAEP 645
QY 691 FATVCTARYVLLSAGSLAFSGFMFATYRVHRIFTR--TGSVFQDKMLQDQLILLVGLL 749
Db 646 GAAVCAARLEFLGLTGLTSYALLTKTNRIYRIFEQGRKSVTPFPISPTSQLVITFSLT 705
QY 750 LVDALLVTLWVTDPMERHLNLTLEISATDRSVVYQPOVE--VCRSQTOTWLSVLAYK 808
Db 706 SIQVGIITWLGARPP-----HSV--IDYEQRTVDEQARGVLCMDSLSLGICLGYS 758
QY 809 GLLLVGVYTMATRHKIPALNDSQYIGSVYSV-VITSAIVVVLNLI--SERVTLAF 865
Db 759 LLLWVTCTVYAIKARGVP-ETFEAKPIGFTMTYTCIWLAFVPIFGTAQSAEKIYQT 817
QY 866 IITAILLSTATLCLLPKPKLHDW 892
Db 818 TLTVSLSLSASVSLGMFYVPKTYVIF 844

RESULT 5

US-08-617-785-14
; Sequence 14, Application US/08617785E
; Patent No. 6228610
; GENERAL INFORMATION:
; APPLICANT: Flor, Peter J.
; APPLICANT: Kuhn, Ranier
; APPLICANT: Lindaur, Kristen
; APPLICANT: Puttnner, Irene
; APPLICANT: Knopfel, Thomas
; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 922
; TYPE: PRT

; ORGANISM: Homo sapiens
US-08-617-785-14 *

Query Match 5.3%; Score 353.5; DB 4; Length 922;
Best Local Similarity 19.5%; Pred No. 1.7e-22;
Matches 201; Conservative 165; Mismatches 37; Indels 291; Gaps 40;

QY 148 RNHGKIVLLGLFELSTSRGP-----RPDGLSLGAATMAVEHNR-KRLLPGYTL- 196
Db 44 RIEGDTLGLLFPVH-AKGPSPVCGDIKRENGIHRLEAMLYALDQINSDPNLLPNVTLG 102
QY 197 -----ELVNTQCDPGVGVDRFFHAIYTOPSTRMVMMLG 231
Db 103 ARILDCSRDITYALEQSLTFVQALIKQKOTSDVRCTNGE-----PPVFKPE-KVVGIG 155
QY 232 SACSEVTESLAKVVPYWNIVOVSGSTSPALSDREFFPYEYRTVAPDSSHNPARIAFIRK 291
Db 156 ASGSSVSIMVANILRLFIQISYASTAPELSDRRYDFRSRVVPDPSFOAAMVDIVA 215
QY 292 FGWGTVTTFSSQNEEVHSLAVNNLVTLEAANISCAATITFAATDFKEQLL-----LL 343
Db 216 LGWNVSTLASGSGYCEKVESFTQISKAGGLCIAQSVIRPQERKDRITIDFRIKQLL 275
QY 344 RETDRIIIGSFSQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHELO 403
Db 276 DTPNSRAVVIFANDEDIKILAAAKRADQVG-HFLWVGSDSWGSKINP-----LHQHE 327
QY 404 LAVENLIVVSTHNSIVGNVSYSGLNHMFNSQLKQSAQFHGQDGFSGYCPRIASIAAT 463
Db 338 DIAEGAITQPKRATV-----EGFDAYFTSRTLENNRNWFAEYWEENFNCKLTISGS 381
QY 464 QSDSRRRRRRGVGTSGGHLFPEAI---SOYAPQ-----TYDAVMAIALARAAEHWR 515
Db 382 KKEDTRCKTG-----QERIGKOSNYEQEGKVQFVIDAVYAMAHAL-----HHMK 427
QY 516 N-----EQSKLDGFDYTRSDMAWEFLQMGKHLFLGVSG-PVSFS-GPDVGTGTA 564
Db 428 DLCADYRGVCPMEQAGG-----KLLKYIRNVNENGSAQTPVMFNKNGDAPGRYD 478
QY 565 FYQIQ-----RGL----- 572
Db 479 IFQYQYTTNTPNGYRLIGOWTDELQNLNEDMOMGKGVREIPASVCTLPCKPGQRKKTQK 538
QY 573 -----LEPVALYYPATDALDFRCPRC---RPVKWHSQ--OVPIAKRVEKLRVATIAPL 620
Db 539 TPCCWTCPCDGYQYQFD--EMTCQHCYDQRPENRRTGCDIPIKLEWHSPWAVIP-- 594
QY 621 AFYTIATLSSVGIATAITFLAPNLHFRKRLKAIKLSPPKLSNITAVGCFIVYATVILLGLD 680
Db 595 -----VFLAMLGIIATIFVMATFIYNDTPIVRASGRELSYVLLTGIFLCYIITFLM--- 646
QY 681 HSTLPSAEDSFATVCTARYVLLSAGSLAFSGFMFATYRVHRIFTR--TGSVFQDKMLQDI 739
Db 647 -----IAKPDVA--VCSFRVFLGLGMCISYAALLTKTNRIYRIFEQGRKSVTAPRLISP 700
QY 740 QLILLVGLLVDALLVTLWVTDPMERHLNLTLEISATDRSVVYQPOVE--VCRSQT 797
Db 701 SOLAITSLISVQLLGVFIWFGVDP-----PNIIDY---DEHKTWNPEQARGVLCMDIT 752
QY 798 QTWLSVLYAYKGLLVGVYMAWETRHVKIPALNDSQYIGSVYSV-VITSAIVVVLNLI 856
Db 753 DLQIICSLGYSILLMVTCTVYAIKTRGV-ENFNEAKPIGFTMTYTCIWLAFIPIFGT 811
QY 857 I--SERVTLAFITITALLTSTATLCLLPKPKLHDWNRNDIIPVHSMGLKMECNTR 914
Db 812 AQSAEKLYIQTTTLTISMNLSASVALGMLYMPKVII-----IFHP----- 852
QY 915 RFVVDRELOYRVVEQNVYKKEIQALDAEIRKLERLLESLTTSITTSSTSLTGG 974
Db 853 -----ELNVOKRRSRFVVTA----- 869
QY 975 GHLKPELTVTSGISQTPAASKN---RTPSIGILPNLLSLVLPVPIPRASWPSPAEMYQIP 1031

; Sequence 2, Application US/08407875
; Patent No. 5912122
; GENERAL INFORMATION:
; APPLICANT: Dagget, Lorrie
; APPLICANT: Lu, Chin-Chun
; TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTOR
; SUBTITLE OF INVENTION: SUBTYPE mGluR6, NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,875
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9921
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 877 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-407-875-2

Query Match 5.5%; Score 372; DB 2; Length 877;
Best Local Similarity 21.6%; Pred. No. 3.2e-24;
Matches 187; Conservative 132; Mismatches 364; Indels 182; Gaps 30;

QY 151 GKIVLLGLFEL-----STSRGP--RPDGLSELGAATMAVEHINR-KRLPG----- 193
DB 37 GGLTLGLFPVHARGACRACGKPLKKEQVHLEAMLYALDRVNDADPELLPGVRLGARLL 96

QY 194 -----YTLELVNTDQC-----DPGVGVDRFFHAIYTOPSTRMVLMLGSCSEV 237
DB 97 DTCSRDTVALQALSFVQALIRGRGDGDEVGVRCGPGVPPLRPAPPERRVAVVGASASSV 156

QY 238 TESLAKVVPYNNIVQVSGTSPALSDRRFPYFRTVAPDSSHNPARIAFKFGWGV 297
DB 157 SIMVANVLRLEAIPQISYASTAPELSDTRYDFRSVVPDPDSYQAOAMVDIVRALGNV 216

QY 298 TTFESQNEEVHSLAVNNLV-TELEAANISCAATITTAAT----DFKEQLLLRETDRII 352
DB 217 STLASEGNYGSGVEAFVQISREAGGVCIQSIKIPREPKEGFEFSKVIIRRLMETPNARGI 276

QY 353 GSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPPDQRTACSNHELQLAVALNLI 412
DB 277 IIFANEDDIRVLEAARQANLTGHLWVGSDSWGAKTSP-----ILSLEDVAVG 325

QY 413 STHNSIVGNVSYGLNNHMFNSQLKSAQPHQDGFSGYGPRIATAATSDSRRRR 472
DB 326 AII--TILPKRASIDGDFQYFMTSRLENRNRIWFAEFWEENCKLTSSGTSQSDSDTRK 383

QY 473 RGVVGTSGCHLFPPEAISQYAPQTY-----DAVNAIALAAEE-----HWRNE 517
DB 384 TG-----EERIGR--DSTYBQEGKVQFVIDAVYAIHAIALHSMHOALCPGHTGLCP 431

QY 518 EQSKLDGFDYTRSDMAWEFLQOMGKHLFLGVSG-PVSFS-GPDRVGTATFYQIQ----- 569
DB 432 AMEPTDG-----RMLLOYIRAVRFNGSAGTVPVNFENGDAPGRYDFYQATNGSA 482

QY 570 -----RGLLEPVALYY 580
DB 483 SSGGYQAVGOWAETLRDLDEALQWSDPHEVPSLCLPCGPGGERKKMWKGV--PCWCWHC 540

QY 581 PATDAL-----DFRCPRC-----RPVKWHSQGVPIAKRVFKLRVATIAPLAFYTIATLSSV 631
DB 541 EACDGYRFQVDEFTCEACPGDMRPTNHTGCRPTP-----VVRLSWSSPWAAPPL-LLAVL 595

QY 632 GIALAITFLAFNLHFRKLKAIKLSPPKLSNITAVGCIFFVATVILLGLDHSITLESADSF 691
DB 596 GIVATTTVATFVRYNNTPIVRASGRELSVLLTGIFLIYAITFLM-----VAEPG 646

QY 692 ATVCTARVILLSAGFSIAGFSGMFATYRVHRIPTR-TGSVFKDKMLQDIQILILVGGILL 750
DB 647 AAVCAARRLFLGLTTLUSYALLTKTNIYRIEFGGRSVTPPPFIPTSOVLVTFSLTS 706

QY 751 VDALLVTLVWVTPDMERHLHNLILEISATDRSVVYQPVQVE-VCRSQHTQTWLSVLYAYKG 809
DB 707 LOVVGMIAWLGARPP-----HSV---IDYEQRTVDPEQARGVLKCDMSDLSLCLGYSL 759

QY 810 LLLVGVYMAWETRHVKIPALNDSQYIGSVYSV-VITSIAIVVVLANLI--SERVTIAFI 866
DB 760 LLMVTCTVYAIKARGVP-ETFNEAKPIGFTMYTTCIIWLAFVPIFFGTAQSAEKIYIQT 818

QY 867 TITALIITSTATILCLLFIKPLHDI 891
DB 819 TLTVSLSLASVSLGMLYVPKTYVI 843

RESULT 4
US-09-126-280-2
; Sequence 2, Application US/09126280
; Patent No. 6103524
; GENERAL INFORMATION:
; APPLICANT: Wu, Su
; APPLICANT: Belagaje, Rama M
; TITLE OF INVENTION: Metabotropic Glutamate Receptor Protein and Nucleic
; FILE REFERENCE: Sequence List
; Patent No. 6103524
; CURRENT APPLICATION NUMBER: US/09/126,280
; CURRENT FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 877
; TYPE: PRT
; ORGANISM: Human
; US-09-126-280-2

Query Match 5.5%; Score 371; DB 3; Length 877;
Best Local Similarity 21.5%; Pred. No. 4e-24;
Matches 186; Conservative 133; Mismatches 364; Indels 184; Gaps 30;

QY 151 GKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLPG----- 193
DB 37 GGLTLGLFPVH-ARGAAGRACGQKKEQGVHREAMLYALDRVNDADPELLPGVRLGARL 95

QY 194 -----YTLELVNTDQC-----DPGVGVDRFFHAIYTOPSTRMVLMLGSCSE 236
DB 96 LDTCSDRTYALEQALSFVQALIRGRGDGDEVGVRCGPGVPPLRPAPPERRVAVVGASASS 155

QY 237 VTESLAKVVPYNNIVQVSGTSPALSDRRFPYFRTVAPDSSHNPARIAFKFGWGT 296
DB 156 VSIWVANVLRLEAIPQISYASTAPELSDTRYDFRSVVPDPDSYQAOAMVDIVRALGNV 215

QY 297 VTFESQNEEVHSLAVNNLV-TELEAANISCAATITTAAT----DFKEQLLLRETDRII 351
DB 384 TG-----EERIGR--DSTYBQEGKVQFVIDAVYAIHAIALHSMHOALCPGHTGLCP 431

[illegible]

RESULT 2

US-09-183-253-4

; Sequence 4, Application US/09183253

; Patent No. 6043054

GENERAL INFORMATION:

APPLICANT: VAWTER, LISA

;

```

1  APPLICANT:  STAMMERS, MELANIE
2
3  TITLE OF INVENTION:  NOVEL COMPOUNDS
4
5  NUMBER OF SEQUENCES:  4
6
7  CORRESPONDENCE ADDRESS:
8
9  ADDRESSEE:  Ratner & Prestia
10
11 STREET:  P.O. Box 980
12
13 CITY:  Valley Forge
14
15 STATE:  PA
16
17 COUNTRY:  USA
18
19 ZIP:  19482
20
21 COMPUTER READABLE FORM:
22
23 MEDIUM TYPE:  Diskette
24
25 COMPUTER:  IBM Compatible
26
27 OPERATING SYSTEM:  DOS
28
29 SOFTWARE:  FastSeq for Windows Version 2.0
30
31 CURRENT APPLICATION DATA:
32
33 APPLICATION NUMBER:  US/09/183,253
34
35 FILING DATE:  30-OCT-1998
36
37 CLASSIFICATION:
38
39 PRIOR APPLICATION DATA:
40
41 APPLICATION NUMBER:  9817907.0
42
43 FILING DATE:  17-AUG-1998
44
45 APPLICATION NUMBER:  60/075,306
46
47 FILING DATE:  20-FEB-1998
48
49 ATTORNEY/AGENT INFORMATION:
50
51 NAME:  Prestia, Paul F
52
53 REGISTRATION NUMBER:  23,031
54
55 REFERENCE/DOCKET NUMBER:  GP-70395
56
57 TELECOMMUNICATION INFORMATION:
58
59 TELEPHONE:  610-407-0700
60
61 TELEFAX:  610-407-0700
62
63 TELEX:  846169
64
65 INFORMATION FOR SEQ ID NO:  4:
66
67 SEQUENCE CHARACTERISTICS:
68
69 LENGTH:  332 amino acids
70
71 TYPE:  amino acid
72
73 STRANDEDNESS:  single
74
75 TOPOLOGY:  linear
76
77 MOLECULE TYPE:  protein
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79 US-09-183-253-4

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Query Match	8.8%;	Score 588.5;	DB 3;	Length 332;
Best Local Similarity	36.7%;	Pred. No. 1.7e+44;		

Sequence similarity	Accession no.	Length	Matches	Mismatches	Indels	Gaps
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100%	U00097	100	100	0	0	0
100%	U00098	100	100	0	0	0
100%	U00099	100	100	0	0	0
100%	U00100	100	100	0	0	0
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Qy	521	KLOGFDYTRSDMAWEFFLOQMKLHFLVGSQPVSGSDRVRGTTAFYQIORGLLEPVVALY	580
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Qy	581	PATDALOFRCPRCPVWHSCQVPIAKRVFKLVAVTIATLPSVGTALAITFL	640
Db	61	AVADTLRIIND--TIRFOGSEPPKDKTIIQLQRKISLPLYSILSALTILGIMASAEFL	117
Qy	641	AFNLHFELKKAIKLSSPKLSNITAVGCIFFYVAVTIIIGLDHSTPLSAEDSFATVCTARY	700
Db	118	FFN1KRNQKLIIMSSYPMNNLILGGMLSYASITFLGDLGSEV--SEKTFELCTFVRTW	175
Qy	701	LLSAGFSLAFSGFEAKTYRHRIFTRTGSVFKDKMLQDIQLILLVGLGLLVDAALLTVLW	760
Db	176	ILTGYGTYTAFCAFEAKTRVHAIFKNV--KMKKKIKDKQLLVIVGMLLIIDLILICHQ	233
Qy	761	VTDPMERHLNLTLEISATDRSVVYQPVQVECRSHQTQTWLSVLYAYKGLLVVGYMAW	820
Db	234	AVDPLRRTVKEYSMEPPDAGRDISIRPLEHCENHTMTIWLGVYAYKGLMLFGCFLLAW	293
Qy	821	ETRHVKIPALNDSQYIGCVSYVSVVITS	847
Db	294	ETRNVISIPALNDSKYIGMSYINVGIITS	320

RESULT 3
US-08-407-1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2002, 10:04:59 ; Search time 26.74 Seconds
(without alignments)
1098.235 Million cell updates/sec

Title: US-09-715-962-6

Perfect score: 6705

Sequence: 1 MKIIQPVQTRYGPWPAVGL.....RLSLGDSQEEQQAPANGTE 1305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	976	14.6	859	3	US-09-183-253-2
2	588.5	8.8	332	3	US-09-183-253-4
3	372	5.5	877	3	US-08-407-875-2
4	371	5.5	877	3	US-09-126-280-2
5	353.5	5.3	922	4	US-08-617-785-14
6	349.5	5.2	915	4	US-08-617-785-12
7	348.5	5.2	915	1	US-08-453-882-2
8	348.5	5.2	915	2	US-08-452-734A-2
9	348.5	5.2	915	4	US-08-176-401B-2
10	348.5	5.2	915	5	PCT-US94-14989-2
11	347	5.2	912	4	US-08-617-785-2
12	340.5	5.1	872	3	US-08-337-797A-2
13	340.5	5.1	872	3	US-09-258-523-2
14	339	5.1	867	4	US-08-617-785-4
15	336.5	5.0	908	4	US-08-855-146-2
16	336	5.0	912	5	PCT-US91-09422-19
17	328.5	4.9	908	3	US-08-823-110-1
18	328.5	4.9	908	3	US-08-604-298-1
19	324	4.8	1219	2	US-08-687-289A-6
20	323	4.8	879	1	US-08-072-574-6
21	323	4.8	879	1	US-08-486-270-6
22	323	4.8	879	3	US-08-367-264-6
23	262	3.9	1059	4	US-09-134-513-2
24	257.5	3.8	1199	1	US-08-041-538-2
25	257.5	3.8	1199	1	US-08-463-642-2
26	257.5	3.8	1199	1	US-08-455-602-2
27	257.5	3.8	1199	2	US-08-465-157-2

28	257.5	3.8	1199	5	PCT-US91-09422-2	Sequence 2, Appli
29	243.5	3.6	1056	2	US-08-687-289A-7	Sequence 7, Appli
30	242	3.6	1194	4	US-08-538-526-1	Sequence 1, Appli
31	240	3.6	1085	1	US-08-485-588-5	Sequence 5, Appli
32	240	3.6	1085	1	US-08-484-565-5	Sequence 5, Appli
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34	240	3.6	1085	2	US-08-943-986-5	Sequence 5, Appli
35	240	3.6	1085	3	US-08-353-784-5	Sequence 5, Appli
36	240	3.6	1085	3	US-08-484-719B-5	Sequence 5, Appli
37	237	3.5	906	5	PCT-US91-09422-17	Sequence 17, Appli
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41	237	3.5	1078	2	US-08-943-986-7	Sequence 7, Appli
42	237	3.5	1078	3	US-08-353-784-7	Sequence 7, Appli
43	237	3.5	1078	3	US-08-484-719B-7	Sequence 7, Appli
44	233.5	3.5	1088	1	US-08-485-588-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P. O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-2

Query Match 14.6%; Score 976; DB 3; Length 859;
Best Local Similarity 27.8%; Pred. No. 1.1e-78;

Search completed: April 30, 2002, 10:06:25
Job time: 393 sec

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 Db 842 -----ILAAFGLLACIFFFNKVYIILFKPSRNTIE-----VRCSTAAHAFKVA 885
 Qy 920 DRRELOYRVEQNRVYKKEIOALDAEIRKLERLLESGLTTTSTTSSSTSLITGGGHLKP 979
 Db 886 ARATLR-----KSNVSRORSSSLGG-----STGSTPSSSISSKSNSEDPFP 926
 Qy 980 ELTVTSGISQTPAASKNRTPTSGILPNLLSVLP-----PVIPRASWPSAEYMOIPM 1032
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 Qy 1033 RR-----SVTFA---SQPO-----LEEACLPADQDILNLRLAHO-----1062
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 Qy 1063 --QATEAKTGL 1071
 Db 1029 DSELTQETGL 1039

RESULT 15

A56715
 calcium receptor (clone pHCar-4.0) - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
 C;Accession: A56715; S49341; A49419; B49419; C49419
 R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.
 J. Biol. Chem. 270, 12919-12925, 1995
 A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor
 A;Reference number: A56715; MUID:95279439
 A;Accession: A56715
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1078 <GAR>
 A;Cross-references: GB:U20759; NID:6683744; PIDN:AA86503.1; PID:9683745
 R;Pearce, S.H.S.; Thakker, R.V.
 submitted to the EMBL Data Library, August 1994
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 A;Status: preliminary
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 A;Cross-references: EMBL:X81086
 R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,
 Cell 75, 1297-1303, 1993
 A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemia
 A;Reference number: A49419; MUID:94094324
 A;Accession: A49419
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 178-192 <POL>
 A;Experimental source: family N
 A;Note: sequence inconsistent with nucleotide translation
 A;Note: sequence modified after extraction from NCBI backbone
 A;Note: 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and ne
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 A;Status: preliminary
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 A;Experimental source: family E
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 A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
 A;Accession: C49419
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 788-802 <PO3>
 A;Experimental source: family J
 A;Note: sequence modified after extraction from NCBI backbone

A;Note: 796-Trp mutation is associated with familial hypocalcemic hypercalcemia and
 A;Note: sequence extracted from NCBI backbone (NCBIN:142457)
 C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 3.5%; Score 237; DB 2; Length 1078;
 Best Local Similarity 19.9%; Pred. No. 4e-08;
 Matches 201; Conservative 141; Mismatches 373; Indels 296; Gaps 44;

Qy 143 PAEMQRNHRGIVILGLFEL-----STSRGPRPD-----GLSELCAATMAVEHI 185
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 Qy 186 NRK-RLLPQVYTLVLTNDTQCD-----PGVGVDFFHAIYTOPSTRM 226
 Db 82 NSSPALLPNLTGLVRIEFT-CNTVSKALEATLSFVAQNKIDSLNDFCNCSEHIPST-- 138
 Qy 227 VMLLGSACSEVTESLAKVVPYWNIVQVSGSTSPALDRREFFYPYRTVADSSHNARI 286
 Db 139 IAVVGATGSGVSTAVANLLGLFYIPOVSYASSRLLSNKQKFSRLTIPNDEHQATAMA 198
 Qy 287 AFIRKFGWGTVTTFSONEEVHSLAVNNLVTLEAANISCAATITFAATDFKEQL----- 340
 Db 199 DIIEYFRNWNVGTIAADDDYGRPGIEKFEREAEERDI-----CIDFSELISQYSD 249
 Qy 341 -----LLLRDTTRIIIGSFSEQLAPQILCEAYRLRMFGADYAWILHESMGAPWMPD 392
 Db 250 EEIQHVVEVIQNSTAKVIVVFSSGPDLEP-LIKEIVRNITGK-IWLASEA-----W- 299
 Qy 393 QRTACSNHLEQLAVENLIVVSTHNSIVGNVNSYS-----GLNHHM-----F 433
 Db 300 -----ASSLIAMPQVHVVGTTGTFALKAQIPGREFLKKVHKPRKSVHNGF 347
 Qy 434 NSOLRKOSAOFHGQDG-----FCSGY--GPRISIAATQSDSRRRRRRGVVGSGG 481
 Db 348 AKFEWEETFNCHLOEGAKGPLVDVTFLRGHEESGDRFSNSTAPRPL-----CTGD 398
 Qy 482 HLFPEAISQYAPQF-----YDAVWAIALALR-----AAEEHW 513
 Db 399 ENISSVETPIDYTHLRISYNYLAVYSIAHALQDIYVCLPGRGLFTNGSCADIKKVEAW 458
 Qy 514 RNREEQSKLD-----GFDY-----TRSDMANEFLOQM----- 541
 Db 459 QVLKHLRLHLAFNNMGQVTFDEGDLGVNYSIINWHLSPEDGSIVFKEGVYNYAKKG 518
 Qy 542 -----KLHFLGVSGPVPSFGPDR--VGTTFAYIOIQRGLLE-----PVAL 578
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 Db 677 CLRQPAFGISFVLCISCLLVKTRNRLVLLVFEAKIPTSFHRKRWGLNLQFLLVLCFTFMOI 736
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Db 311 DVTGQYRE-AVGSIITIKLQSPDKWFDYLLKLRLPETNLRNPNWFQFQWHRFOCRU--- 366
QY 441 SAQFHQDGF---GSGYGPRIATAQSDSRRRRRRVGTSGHLPEAISQAPOTYD 497
Db 367 -----EGFAQNSKYN-----KTCNSSLTLRTHVQSKMGFVI-----N 401
QY 498 AVMAIALRAAEHRRNEEQSKLQGF---DYTRSDMAWEFLQOMKHLFLGVSGPV- 552
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QY 553 -----SFGSGPDR-----VGTTFAYQIQRG-----LLEP 575
Db 454 LFDENGDSFGRYIMNFKEKMGKDYFDYINGSWDNGELKMDDEWVKNNIIRSVCSPE 513
QY 576 -----VALYYPATDAL-----DFRCPRCPVKWHSQG-----VPIAKRV 609
Db 514 CEKGQIKVIRKGVSCWCTPCKENEYVEFDEYTCACKQLGSMPTDGLTGDLIPVQ--- 570
QY 610 FKLRVATIAPAFYTTATLSSVGLAITLAFNLHFKLKAIKLSSPKLSNITAVG-CI 668
Db 571 -YLRWGDPEPIAAVFACL---GLLATLFVTVIIFIIDTPVVKSSRELCYIILAGICL 626
QY 669 FVATVILLGLDHLSTLPSAEDSFATVCTARVYLLSAGFSL---AFGSMFAKTVYHRIF 724
Db 627 GYLCTFLI-----AKPQIYCYLQRIQIGLSPAMSYSAIYKTKNRIARIL 672
QY 725 TRFGSVFKDK---MLQDIQLILLVGLLLVDALLVTLVWVTPDPMERHLNHLTLEISATD 780
Db 673 AGSKKICKTKPRFMSACQLVIAFLICIQGLIIVAFIMEPPDIMHDPYSIREVYL-- 730
QY 781 RSVVYQPOVEVCRSQHTQWLSVLYAYKGLLLVGVYMAWETHVKIPA-LNDSQYIGVS 839
Db 731 -----ICNT---TNLGVVTPLYGULLILSCTFYAEKTRNV--PANFNEAKYIAFT 776
QY 840 VYXSV-VITSAIVVLANLISERVITAFITILITLITSTATLCLLFTPKLHDWARNDII 898
Db 777 MTTCTIILWIAFVPIYGSNKIITMCF---SVLSATVALGC-MFVPKVYIILA----- 826
QY 899 DPVIHSMGLKMECNTRFRVDDRELOQRYVEQVONRYKKEIQALDABIRKLERLLESLT 958
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QY 959 TWS---TTTSSSTSLITGGHLKPELTV-----TSGISQTPAASKNRPSPIS--- 1002
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QY 1003 GILPNL-----LLSVLPVPIPRASWPSAEYMQIPMRRSVTFASOPOLEACUPAQDLI 1055
Db 935 GSGPGVAGAGNACCTATGPEPPDAG-PRALYDVAEAESEFPAAARSPSPFI----- 986
QY 1056 NLRLAQQAQTEAKTGLINLRGIFSRITSSNKGSTASLADQKGLKAAFKSHMGLFTRLIP 1115
Db 987 -STLSHLAGSAGRTD--DDAPLSHSETAARSSSSQGSIMEQ-----I 1025
QY 1116 SSGTASCNAIYNPNQDPSIPSEASSHPNGNHLKPIIRGSLTKSGTHL-DHLTKDPNELPI 1174
Db 1026 SSVVTRFTANISELNSMMLSTAATGPPPGT---PICSSYLIPKEIQIPLTTMTTFAEIQPL 1082
QY 1175 PRTI--SGGFGQDQTLGGKVKVLLKLVNFKVLPNRRRPSVVQO---PPLRERVGRSPRP 1229
Db 1083 PALEVTTGAQOQ-----ATGVS---PAQETPTGAESAPGRDLEELVALTPPSP 1127
QY 1230 HR 1231
Db 1128 FR 1129

RESULT 14

S40476

Ca(2+)-sensing receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Nov-1999

C:Accession: S40476

R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.
Nature 366, 575-580, 1993
A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor fro
A:Reference number: S40476; MUID:94077182
A:Accession: S40476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1085 <BRO>
A:Cross-references: GB:S67307; NID:9453108; PIDN:AAB29171.1; PID:9453109

Query Match 3.6%; Score 240; DB 2: Length 1085;
Best Local Similarity 20.0%; Pred.No.2.5e-08;
Matches 230; Conservative 153; Mismatches 412; Indels 356; Gaps 53;

QY 143 PAEMQRHGKIVLLGLFEL-----STSRGPRPD-----GLSLGAATMAVEHI 185
Db 23 PDQRAQKGGDIILGGLFPIHFGVAVKDDQLKSRPESVEICIRYFRGFWLQAMIFAIEI 82
QY 186 NRK-RLLPGYILELVTNDTQCD-----PGVGVDFFHAIYTOPSTRM 226
Db 83 NSSPALLPNMTLGYRIFDT-CNTVSKALEATLSFVAQNKKIDSLNLDKFCNCSEHIPST-- 139
QY 227 VMLGGSACEVTESLAKVVPYNNIVQVSGSPALSDRRPEPYRTVAPDSSHNPARI 286
Db 140 IAVGATGSGISTAVANLLGLFYIFQVSYASSRLLSNKKQPKSFRLTIPNDEHOATAMA 199
QY 287 AFIRKFGGTVTTFQSENEVHSLAVNNLVLEAANISCAATITFAATDFKQL----- 340
Db 200 DIIIEFRNNWGTIAADDYGRPGIEKPREAEERDI-----CIDFSLISQYSDE 250
QY 341 -----LLRETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWMPD 392
Db 251 EKIQQVVEVIONSTAKVIVWFSSGPDLEP-LIKEIVRRNITGR--IWLASEA-----W-- 300
QY 393 QRTACSNHELQAVENLIVVSTHNSIVGNVYSGLN-----NRM 432
Db 301 -----ASSLIAMPEYFHVVGTTGF-GLKAGQIPGPREFFLOKHPKRSVHNG 347
QY 433 FNSOLRKQSAFHQDQG-----FGSGY---GPRISIAATQSDRRRRRRRVVGTSG 480
Db 348 FAKFEWETFNCHLQEGAKGGLPVDFFLHGEEGARLSNSPT---APRPLCTGENISS 404
QY 481 -----GHLPPEAISQYAPQTYDAVMAIALALR-----AAEEH 512
Db 405 VETPYMDYTHL-----RISNVYLAVYSIAHALQDIYTCIPGRGLFTNGSCADIKKVEA 458
QY 513 WRNREEQSKLD-----GFDYTRSDMA-----WEFLQOMG----- 541
Db 459 WQVLKHLRLHFTSNMGEQVTFDEC-GDLAGNYSIINHLSPEDEGSIVFKEVGYNNYAK 517
QY 542 -----KLHFLGVSGPVSGPDR---VGTTFAYQIQORLLE-----PV 576
Db 518 KGERLFINDEKILNSGFSREVPFNSCRDCLAGT-----RKGIIEGEPTCCFEVCEPD 571
QY 577 ALYYPATDALDFRCRCRPVKW---HSGQVPIAKRVFKLRVATIAPAFYTIATLSSVG 632
Db 572 GEYSDETDA--SACDKCPDDFWSNENHTS--CIAKEIEFLSWTEPFGIALTLFAVL--G 624
QY 533 IALAITFLAFNLHFKLKAIKLSSPKLSNITAVGCIYFATVILLGLDHLSTLPSAEDSEA 692
Db 625 IFLTAFVLGVFIKFRNTPIVKATNRELSYLLLSLFCGSSSLFF-----IGEPQD--- 675
QY 693 TVCTARVYLLSAGFSLAFGSMFAKTVYHRIF-TRTGSVENDKMLQDIQLILLVGLLLV 751
Db 676 WTCRLQPAFGISFVLICISILVKTNRVLLVFEAKIPITSFHRKWWGLNQLQFLVFLCTFM 735
QY 752 DALLVTLWVVTDPMERHL-HNLTLEISATRSVVYQPOVEVCRSQHTQWLSVLYAYKGL 810
Db 736 QIVICAIWLNTPAPSSYNHELEDEI-----IFITCHEGSLMALGFLIGYTC 783
QY 811 LLVGVGVYMAWETHVKIPA-LNDSQYIGVS--VYSVWITS---AIVVLANLISERVTLA 864

Nature 349, 760-765, 1991
A:Title: Sequence and expression of a metabotropic glutamate receptor.
A:Reference number: S15362; MUID:91156047
A:Accession: S15362
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1199 <MAX>
A:Cross-references: EMBL:X57569; NID:g56646; PID:g56647
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	3.8%;	Score 257.5;	DB 2;	Length 1199;
Best Local Similarity	19.9%;	Pred. No. 1.7e-09;		
Matches 249;	Conservative 171;	Mismatches 459;	Indels 375;	Gaps 57;

Qy	120	LNLPPRQRYUKVNOVFSESRMSPAEMORNHGKIVILGLFELSTSRGPRD	-----	170	
Db	16	MSILPRMPDRKVLLAGASSOR	---SVARMGDVVIIGALF---SVHHQPPAEKVPKRCGE	69	
Qy	171	-----GLSELCATMAVEHNRKR	-LLPGVTLELVNTDQC-----	205	
Db	70	IREQYGQORVEAMPHUDKINADPVLLPNITLGEIRDS	-CHWSVALSQSIEFIRDSLI	128	
Qy	206	---DPGCVDRFFHAIYTOPSTR	---MVMLLGSAGSEVTESLAKVVPYWNVIQVSFGST	258	
Db	129	SIRDEKDLNRLCPDGQTLPPGRTKPKIAGVIGPGSSVAIQVOLLQFLDPIQAYSAT	188		
Qy	259	SPALSDRRPPYFYRTVAPDOSSHNPARIAPIRKFGMGTVTTFSSQNEEVHSIAVNNLVTEL	318		
Db	189	SIDLSDTLKYFLURVVPSTLQARAMDITVKKRYN	-TVVSAVHTGNTGESGMDAFKEL	247	
Qy	319	EAANISCAAITFAATOFKOLL	-LLRENDTRI---IIGFSQELAPQILCEAVR---	369	
Db	248	AAQEGLCIAHSDKIYSNAGEKSFDRLLKURERLPRKARVVVCEGTVRGLLSAMRRUG	307		
Qy	370	---LRMGADYAWI	-----LHESMGAP	388	
Db	308	VVGFEFLIGSD	-GWADRDEVIEGVEANGGITIKLQSPEVRSFDDYFLKLRLDTRNRP	366	
Qy	389	WWPD	---QRTACSNHEIQLAVENLIVYSTINSIVGNVSYSGUNNIMFNSQLRKSQAQPH	445	
Db	367	WFPEFWHRFCQRLPGHLLNPNFKVCTGNESLEENYQDSKMGFVINAIY	-----AMAH	422	
Qy	446	QDQFGSGYGB	---RISIAATQSDSRRRR	---RRGVGTSGGHLPEALISQVAPOTYDA	498
Db	423	GLQNNHIALCPGHVGLCDAMKPIDGRKLLDFLKSSFVGSVEEWFDEKGD	-APGRYDI	481	
Qy	499	VWATIALRAAEHRRNEEQSKLDGFDYTRSDMAW	-----EFLQMGKHLFL	-GVS	549
Db	482	M	-----NLQVTEANRYDYVHV	-TWHEGVNLDDYKIQMKNKSGMVRVC	524
Qy	550	GPVSFGPDRVGTTFQIOIGLLEPVALIYPATDAL	-----DFRCPRCPVKHSCQ	602	
Db	525	SEPCLGQOIKV	-----IRKG	---EVSCCWICTACKENEFODEFTCRACDLGMPWPAE	574
Qy	603	V	-----PIAKRVFKLR	-VATIAPLAFYTIATLSSVIGIALAITFLAFNLHFKRLKAIKLSPP	657
Db	575	LTGCEPIPVRYLEWSDIESIIATF	-----SCLGILVTLFVTLIFVLRYDTPVKSSSR	628	
Qy	658	KLSNITAVGCIFFVATVILGLDHSTLPSAEDSFATVCTARVYLLSAGFSIAGSMFAKT	717		
Db	629	ELCYIILAGIFLPGVCPFTLIAKPTT	-----TSCYLQRLVLLGLSSAMCYSALVTKT	679	
Qy	718	YRVHRIFFRTGS	-----VFRDKMLQDILQLILLYGGLLLVD	-ALLYTLVWVTDPMERHLHN	771
Db	680	NRIARIL	-AGSKKKICTRKPFRMSAWAQVIAISILISVQLTIVLWTLIMEPPM	-----	731
Qy	772	LTLEISADRSWVYQPOVE	-----VCRSOHTQWLSVL	-YAYKGLLLVGVYMAWETRVH	825
Db	732	-----PILGYPSIKEWILCNTSN	-----LGVVAPVGYNGLLINMSCTYYAFKTRW	777	
Qy	836	KIPA	-LNDSDQYIGSVYSV	-VITSIAVVIWANLISERVTLAFITITAILITSTATLCLL	883

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Db 778 --PANFNEAKYIAFTWYTCIIWLAEVPIYFGSNYKIITCF-----AVSLSVTVALGC-M 830
Qy 884 FIPKLHIWIARNDIIDPIVHSMGLKMECNTRRFVDDRELQYRVEVQNRVYKKEIQALD 943
Db 831 FTPKMYIIIA-----KERNVR-----847
Qy 944 AEIRKRLLESGLTITSTTTSTSTSLTGGGGHLKPELIVTSGISOTPAASKNRTPSISG 1003
Db 848 -----SAFTTSVVRMHVGDGKL-----PCRS-----869
Qy 1004 ILPNLLSVLPVPIPRASWPSEAEMQIPMRRSVTFASQPQLEEACLPQODLINRLA-HQ 1062
Db 870 ---NTFNIIFRRKKPGAGNANSN-----GKSVSW-SEPGGRQA--PKGQHVQRLSVHV 917
Qy 1063 QATEA---KTGLINLRIGIFSRTTSNKGSTASLADQKGLAAFKSHMGLFTRLIPSSOT 1119
Db 918 KTNETACNOTAVIKPL-----TKSVQSGKSL-----TFSD 948
Qy 1120 ASCNAIYNPNODISPEASHPGNHLKPIHSGSLTKSGTHL-DHLTKD--PNFLPIPT 1176
Db 949 ASTKTLYNVEEDNTPSAHFSPSSPSSVWVHRGPPVATPPPLPHTLAETPLFLASDV 1008
Qy 1177 ISGG-----EQGDQTLGGKYVKLLETKNVQLPNSRRPSVWQPPSLRVRVG 1224
Db 1009 IPKGLPPLPQQQPPQ-----QPPQPP--QPKSLMDQLQG 1043

RESULT 13
A42916
metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A42916
R:Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor
A:Reference number: A42916; MUID:92317054
A:Accession: A42916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1171 <AB>
A:Cross-references: GB:DI0891; NID:9220813; PIDN:BA017111.1; PID:dI002186;
A:Experimental source: brain
A>Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIPI:107750)
;Keywords: G protein-coupled receptor; transmembrane protein

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Query Match 3.8%; Score 256; DB 2; Length 1171;
Best Local Similarity 19.6%; Pred. NO. 2.1e-09;
Matches 247; Conservative 180; Mismatches 513; Indels 322; Gaps 54;

Qy	137	SERMSPAEMORNHGKIVLLGLFELSTSRGPRD-----GLSELGAATMAV	182
Db	23	SERRV----VAHMPGDIIIGALF--SVHHQPTVDKHVERKCGAVREOYGIQRVEAMLHTL	76
Qy	183	EHIRN-KRLLPGYTLELVNTDTCDDPGVGVDREFFAIYT-----	220
Db	77	ERINSDPTLPNIYTLTGCEIRDSCHWSAVALSEQSIEFRDLSISSEEEGLVRCDGSSSF	136
Qy	221	QPSTRMYMLLGCSACEVTESLAKVPVWNIVQVSFGSTSPALSDREFPFYRTVAPDSS	280
Db	137	RSKKPINGVIGSGSSVAIQVNLQLFNIPQIAYSATSMDSLDTLFXFYMRVVPVSDAQ	196
Qy	281	HNPARIAFIRKEGNGTVTTTSQNEVHSVLANNLVTELEANISC AATTTFATDFPKOL	340
Db	197	QARAWDIVKYRNY--TYVSAVTHEGNYGESGMEAFKDMSAKEGICIAHSKYIKYSNAGEOS	255
Qy	341	L--LLRETDTRI----IIGFSQELAPAQILCEAYRURMFCADYAWILLHESMGAPWMPDOR	394
Db	256	FDXLLKLRLSHLPKARVVACFCEGMVTRGLDMA--MRRUGLAGEFLL---LGSDCWADRY	310
Qy	395	TACSNNHELQLAVENTLIVVSTHNSTGVGNVSY-----SGLNN-----HMFNSQLRKQ	440

Db 215 ALKNVYVSTLASGSGVGEAFVOKSRENGVGVIAQSVKIPREPVTGFEFDFKIIKRLLE 274
Qy 346 TDTRIIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHQLOLA 405
Db 275 TSNARGIIIFANEDDIRVLEARRANQTGHFWGSDSWGSKSAPVLR-----LEEV 327
Qy 406 VENLIVSTHNSIVGNVSYSGLNHMFNSQLRKOSAPHGODGFGSGYGPRTISIAATOS 465
Db 328 AEGAV-----TILPKRMSVGFDRYFSRTLDNNRRNIWFAEFWEDNFCKLSRHAKK 381
Qy 466 DSRRRR--RRGVVTSGGHLPEALISQYAPQYDAVWATALALRAAEHW--RRNEEQSK 521
Db 382 GSHKKCTNRERIGODSAY-BOEGKVQF---VIDAVYAMGHALHAMHRDLCPRGVGLCP 437
Qy 522 LDGFDYTRSDMAWEFLQOMGKLHFLGVSQ-PVSFS-GPDRVGTGTAFYQIQRGLLEPVLY 579
Db 438 MDVPGT-----QLLKIRVNFVSGIAGNPVTFNENGDAERYDIQYQV---LRNGSAE 488
Qy 580 YPA-----TDALDFRCPR-----CRP-----VK-----WH----- 599
Db 489 YKVGSTWTDHLHLRTERMQWPGSGQOLPRISCLPCQPCGERKKTVKGMACCWHCEPCTGY 548
Qy 600 -----SGQVPIAKRVFKLRVATAPLAFYTIATLSSVGI A- 634
Db 549 QYQVDRYTCKCPYDMRPTENRTSCQPIPIVLEWDSPPA-VLPL-----FLAVVGI A 601
Qy 635 ---LAITFLAFLNHLPRKKAIKLSPKLSNITAVGICFYATVILLGLDHLSTLPSAEDSF 691
Db 602 TLFVVVFVRYN---DPTIVKASRELSYVLLAGIFLCYATTFM-----IAEPDL 649
Qy 692 ATVCTARYLLSAGSFLAGSMFAKTYRVHRIFTR-TGSVFKDKMLQDILQILLVGGLLL 750
Db 650 GT-CSLRIFLGLGMSISYAALLTKTNRIYRIFEQGRKSVSAPRFTSPASQLAITILIS 708
Qy 751 VDALLVTLWVTDPMERHLNLTLEISATDRSVV-YQPOVE-----VCRSQHTQWTL 801
Db 709 LQLLGICVMFVVDP-----SHSVVDQDQRTLDPRFARGVLYKCDISDLSL 753
Qy 802 SVLYAYKGLLVGVYMAWETRVHKIPALNDQYIGSVYSV-VITSALVVL--ANLIS 858
Db 754 ICLIGYSMLLMWCTVYAIKTRGV-ETFEAKRPGITMITTCIVMLAFIPIFFGYSQSA 812
Qy 859 ERVTLAFTITATILITSTATLCLLFIPLKLDI 891
Db 813 DKLVITQTTTLAVSVLSASVSLGMLYMPKVYII 845

RESULT 10

T27628
hypothetical protein ZC506.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T27628
R;Harris, B.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z20395
A;Accession: T27628
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-999 <WIL>
A;Cross-references: EMBL:Z47073; PIDN:CAA87374.1; GSPDB:GN00028; CESP:ZC506.4
A;Experimental source: clone ZC506
C;Genetics:
A;Gene: CESP:ZC506.4
A;Map position: X
A;Introns: 32/2; 65/3; 77/3; 113/2; 140/3; 177/2; 240/2; 277/1; 315/2; 439/2; 471/3; 591/3
C;Superfamily: metabotropic glutamate receptor 4

Query Match 4.6%; Score 306.5; DB 2; Length 999;
Best Local Similarity 20.1%; Pred. No. 4.7e-13;
Matches 206; Conservative 144; Mismatches 307; Indels 369; Gaps 48;

Qy 118 HLLNLPQRQRYLK-VNOVFESERRMS----- 142
Db 13 HLLN---QQFLDCLNHLFNHYRLSTFQKPPSIIRHMFVSLALAIQILANVNVVAQTTE 68
Qy 143 -----PAEMQ--RNHGKIVILGLFELSTS--RGRPP-----DCLSELGAATMAVEHI 185
Db 69 AVDLAPPKPKVQRIIPGIDILIGGVFVHKSLSNGDEPCGEIATRGVHRVEMALVALDOI 128
Qy 186 NRKR-LLPGYTLELVTDQCPGVGVDFRFFHAY-----TOPSTR-- 225
Db 129 NSQNDFLRGYKLGALILDCSNPAYALNQSLDFVDMTIGSSSEASDYVCLDGDSPDLKKOS 188
Qy 226 ---MVLMLSACSEVTESLAKVVPYMWIVQSFSTSPALSDRREFFYFYFTVAPDSSH 281
Db 189 QKNVAAVVGSGSYSSVQLANLLRLFRIAQVSPASTNADLSKDNRFEFYFARTVPSDDYQ 248
Qy 282 NPARIATIRKFGWGTVT--TFQNE-----EVHSLA 310
Db 249 AMAMVEIAVFKWSYVSLVYSADEYGEIGADAFKREARKKGICIALEBRIQNKKESTES 308
Qy 311 VNNLVTELE-AANISCAATITFAATDFKEQLLLRETDTRIIGSFQELAPQILCEAYR 369
Db 309 INNVLQQLQPEKNVGVATVVILFVGTEYIPD--ILRYTAERMKLTSGAKK---RII----- 358
Qy 370 LRMEGADYAWILHESMGAPWMP---DQRTAGSNHLOLAVENLIVVSTHNSIVGNVSV- 425
Db 359 -----WLASES-----WDRNDKVTAGDN---RLAOGAIVMLASQKVPSEFYF 401
Qy 426 ---SGLNHMFNSOLR-----KOSAFHGODGFGSGYGPRTISIAATOSDSRRRRRGVY 476
Db 402 MSLHPGTEAFERNKWLRELQWKVKEFDTPPG-----STASRCEDIQ----- 445
Qy 477 GTSGLHLPPEAISQYAPQYDAVWALALALR-----AAEEHW-RRNEEQ----- 519
Db 446 STEGFNADDKV--QF---VIDAVYAIAGHLSQMSKQAIQCPDDAIENHWISRSKQPEICHA 500
Qy 520 -SKLDGFDYTRSDMAWEFLQOMGKLHFLGVS----- 551
Db 501 MONTDGSDF-----YQNYLLKVNFTGKTIISFPSSFELSPFDIVGKRFRFSPQGDGP 552
Qy 552 VFSF-----GPDVRGTTAFYQI-----QRGLL-----EPVAL-- 578
Db 553 ASYITLYTKPKSMDKRRMTDDESSPSDYVEIGHNSNNLTIVYKKNLWMDPDHPTVSVCS 612
Qy 579 -----YYPATD---ALDPRCPRC 593
Db 613 LPCKIGFRKQLIKDEQCCWACSKCEDYELINETHCVGCEGGMWPTKDKKGCDFLSLSOL 672
Qy 594 RPVKWHS--GOVPIAKRVFKLRVATIAPLAFYTIATLSSVGIATLAFNHLHFKRLKA 651
Db 673 KYMWRSMYSLVPTILAFVGI-IATLFVIVYVI-----YNETPV 711
Qy 652 IKLSPKLSNITAVGCIIFYA-TVILLGLDHLSTLPSAEDSFATVCTARYLLSAGSFLAF 710
Db 712 VKASGRELSYILLISIMCYCMTFVLL-----SKPS-----AIVCAIKRTGIGFAFSCLY 761
Qy 711 GSPFAKTYRVHRIETRTGVSFVKDKMLQDILQILLVGGLLLVDALLVTLWV-VTDPMERHL 769
Db 762 SAMFVKTNRIEIRIFS-TRSAQRPRFISPIQVVMYMTLAGVQLIGLSLWLSVVPVPCWRHH 820
Qy 770 H---NLTLEISATDRSVVYQPVQVCRSQHTQWTLVSLYAYKGLLVGVYMAWETRVH 825
Db 821 YPRDQVVVLTNCVDPDHHFLYS-----LAYDGLVILCTTYAVKTR-- 860
Qy 826 KIPA-LNDSOYIGSVYS--VVITSALVVLNANLISERVTLAFITATILITSTATLCL 882
Db 861 KVPENETKFIKFSMYTTCVWLSWIFFFGTGSDFQIOTSSLCIS--ISMSANVALAC 918
Qy 883 LFIPKL 888
Db 919 IFSPKL 924

C:Genetics:
A:Gene: mGluR3
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-979/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>
F:577-599/Domain: transmembrane #status predicted <TM1>
F:614-634/Domain: transmembrane #status predicted <TM2>
F:646-664/Domain: transmembrane #status predicted <TM3>
F:689-709/Domain: transmembrane #status predicted <TM4>
F:735-756/Domain: transmembrane #status predicted <TM5>
F:770-791/Domain: transmembrane #status predicted <TM6>
F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 5.0%; Score 336; DB 2; Length 879;
Best Local Similarity 20.1%; Bred. No. 3.2e-15;
Matches 199; Conservative 133; Mismatches 330; Indels 326; Gaps 45;

QY 151 GKTIVLGLFELSTST-----RGRPPD-GLSELGAATMAVEHINRKR-LLPG-----YTL 196
DB 37 GDLVGLGLFPINEKGTGTECRGINEDRGIQRLFAEIMKNDKYLPLPGVRLGVHIL 96
QY 197 ELVTNDT-----QCDPGVGVDRFFHAIYTOPSTFWMLLSGAC 234
DB 97 DTCRSRTYALEQSLFVFRASLTQVDEAYMCPDG-----SYAIQENIPLLIAGVIGSY 150
QY 235 SEVTESLAKVVPYNNIVQVSGFSTSPALSDRRFPFYRTVAPDSSHNPARIARIRFGW 294
DB 151 SSVSIQVANNLLRFQIPQISYATSKLSKSDYDFARTVPPDYQAKMAEILRFENW 210
QY 295 GTVTTFSQNEEVSLSLVANNILVTELEANISCAATITFAATDFKQL-----LLRETDTTR 349
DB 211 TVYSTVASEGDYGETGTEAPEARLNKICIAATAEKVGRSNIKRSYDSVIRELQKPNAR 270
QY 350 IIGSFSQELAPOLCEAYPLRMFGADYAILHESMCA----- 387
DB 271 VVFLMRSDSRELIAAASRV-----NASFTWASDQWGAQESIVKGSBHAYGATILELAS 327
QY 388 -----PWMPD-----ORTACS-----NH-----ELQLAVE----- 407
DB 328 HPVRFQDRFYQSLPNYNHNPFRFWEQKFOCSLQNRHNRHRCIKDLAIDSSNYEQE 387
QY 408 -----NLIVSTH-----NSIVGNVSYSGLNHMFNSQLRKQ-----SAQPHGQ 447
DB 388 SKIMFVNAVYAMAHALHKMORTLCPTNTKLCDAKILDKGLKYKDYLLKINFAPENPN 447
QY 448 DG-----FCSGYGPRIISAATQSDSRRRRRRGVGTSGGHLFPPEAISQYAPQYDA 498
DB 448 KGADSVTKFDTYDGGMG-RYNVFNFOHIGGKYSYLKV-----GH----- 485
QY 499 VMAIALARAAAEHWRNEQSKLDGFDYTRSDMAWEFLQMGKHLFGLVSGPVVSFGPD 558
DB 486 -NAETLYLDVDSLHNSRN----- 511
QY 559 RVGTTFAYQIQRG-----LLEPVALYPAPDALDFRCPRCPVKWH-----SGQVPIAKRV 609
DB 512 PCAPNEMKNQPDGVCWICIPCPEYELVD--EFTCMDCGPGWPADLSGCYNLPEDY 569
QY 610 FLKRLVA-TIAPLAFYIATLSSVIGIALAIT-FLAFNLHFRKLKAIKLSSPFLSNITAVGC 667
DB 570 IRWEDAWAIGPV---TIACLGFMCTCIVITVFKNH---NTPLVKASGRELCYVILFGV 622
QY 668 IFYATVILLGLDHSITLPSAEDSFATVCTARVYLLSAGFSLATGSMFAKTYRVHRIF--T 725
DB 623 SLISYCMTFE-----IAKPS-----PVICALRRLGLGTSFAICYSALTUKTNCIARIDGV 673
QY 726 RTGSGVFKMKMLQDILQILVGLGLLLDALVTLWVYTDPMERHLNHLNLTLEISATDRSVVY 785
DB 674 KNGAQ-RPKFISPSQVFCILGILQIVMVSVLI-----LETPGTRRYTLP 720
QY 786 PQQVEV---CRSQHTQTWLSVLVYKGLLVGVGYMAWETRRHKIPA-LNDSQYIGSVY 841

DB 721 EKRETVILKCNVKDSSMLISL--TYDVLVILCTVYAFKTR--KCPENENKAFIGFTMY 776
QY 842 SVVITSAIVVLANLISERVTLAFITITALILTST-----TATLCL-----LF 884
DB 777 TTCI-----IWLAFLPI--FYVTSDDYRVQVTTMCISVLSGFWVLGCLF 819
QY 885 IPKLHDIWARNDIIDPVVHSMGLKMECNTRFRVVDRELQYRVQVNRVYKKEIQALDA 944
DB 820 APKVHIV-----LFQP-----QKNV-VTHRLH----- 840
QY 945 EIRKLERLLESLTWTSTTTSTSSSTSLT 972
DB 841 ----LNRFSVSGTATYSSOASASTYVPT 864

RESULT 9
JH0563
metabotropic glutamate receptor 4 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-Nov-2000
C:Accession: JH0563; I58149
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0563
A:Molecule type: mRNA
A:Residues: 1-912 <TAN>
A:Experimental source: brain
R:O'Hara, P.J.; Sheppard, P.O.; Thøgersen, H.; Venesia, D.; Haldeman, B.A.; McGrane, Neuron 11, 41-52, 1993
A:Title: The ligand-binding domain in metabotropic glutamate receptors is related to Neuron 11, 41-52, 1993
A:Reference number: I58149; MUID:93332699
A:Accession: I58149
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-123; R, 125-912 <RES>
A:Cross-references: GB:M90518; NID:g205400; PIDN:AAA93190.1; PID:g205401
C:Comment: This protein is coupled to a G protein and evokes a variety of functions b C:Genetics:
A:Gene: GLUR4
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phos F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-912/Product: metabotropic glutamate receptor 4 #status predicted <MET>
F:588-610/Domain: transmembrane #status predicted <TM1>
F:625-645/Domain: transmembrane #status predicted <TM2>
F:657-675/Domain: transmembrane #status predicted <TM3>
F:700-720/Domain: transmembrane #status predicted <TM4>
F:751-772/Domain: transmembrane #status predicted <TM5>
F:786-807/Domain: transmembrane #status predicted <TM6>
F:822-847/Domain: transmembrane #status predicted <TM7>
F:98,301,454,484,569/Binding site: carbohydrate (Asn) (covalent) #status predicted F:621,689,695,859,870/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 5.0%; Score 336; DB 2; Length 912;
Best Local Similarity 22.1%; Bred. No. 3.4e-15;
Matches 193; Conservative 134; Mismatches 346; Indels 200; Gaps 36;

QY 148 RNHGKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLLEPGYTLE 197
DB 44 RIDGDITLGLFPVH-GRGSEKACGKELKEGIHRLAEMLFALDRINDDPLDPLNITLG 102
QY 198 LVTNDTQCDPGVVDVRFHA----- 230
DB 103 ARILDT-----CSRDTHALEQSLTFYQALIEKDGTEVRCGSGGPPITRKE-RVVGVI 154
QY 231 GSACSEVTESLAKVVPYNNIVQVSGFSTSPALSDRRFPFYRTVAPDSSHNPARIARIFR 290
DB 155 GASGSSVIMVANNILRFKIPQISTASTAPDLSNRSYDFFSRVVPVSQYQAQAVDVR 214
QY 291 KFGWGTVTFTSQNEEVSLSLVANNILVTE-LEANISCAATITF-----AATDFEQLLLLRE 345

[illegible]

RESULT 8
JC7160
metabotropic glutamate receptor subtype 3 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C:Accession: JC7160
R:Minoshima, T.; Nakanishi, S.
J. Biochem. 126, 889-896, 1999
A:Title: Structural organization of the mouse metabotropic glutamate receptor
A:Reference number: JC7160; MUID:20012997
A:Accession: JC7160
A:Molecule type: DNA
A:Residues: 1-879 <MIN>
A:Cross-references: GB:AF170696

C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>
F:568-590/Domain: transmembrane #status predicted <TRI>
F:605-625/Domain: transmembrane #status predicted <TII>
F:637-655/Domain: transmembrane #status predicted <III>
F:680-700/Domain: transmembrane #status predicted <TIV>
F:726-747/Domain: transmembrane #status predicted <TRV>
F:761-782/Domain: transmembrane #status predicted <TVI>
F:795-819/Domain: transmembrane #status predicted <VII>
F:203,286,338,402,547/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F:832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.1%; Score 343.5; DB 2; Length 872;
Best Local Similarity 21.6%; Pred. No. 9.5e-16;
Matches 191; Conservative 115; Mismatches 338; Indels 241; Gaps 36;

Qy 151 KRIVLLGLFELSTSRGPRD-----GLSEGAATMAVEHINR-KRLPG----- 193
Db 30 GDLVGLGLFPVHKGGPAECGPVNEHRIQRLLEAMLFALDRINRDPHLLPGVRLGAHIL 89
Qy 194 -----TYLELVNTDTCDPGVGVDRFFH-----AIYQPSTRMVMLLGSACSEVTE 239
Db 90 DCSCKDTHALEQALDFVRASLSRGADSRHICPDGSIATHSDAPTAVTGVIIGSYDSVI 149
Qy 240 SIKAVVPYNNIVQVSGSTSPALSDREFPYFYRTVAPDSSHNPARIAFIRFGWGTVT 299
Db 150 QVANLLRLFQIPQISVASTSAKLSDKRYDYFARTVPDPFQAKMAEILRFNFTWYTVST 209
Qy 300 FQNEEVHSLAVNNLVTELEAANISCAATI-----TFAATDFKEOL-LLLRETDTRIIG 353
Db 210 VASEGDYGETGIEAFLEEARARNI-CVATSEKVGRAMSRAAFEGVVRRALLQPSARVAVL 268
Qy 354 SFSQELAPOLICEAYRLRMFGADYAWILHESMGA----- 387
Db 269 FTRSEDARELLAATQRL--NASFETWASDGGWALESVVAGSERAEGAITTELASYPIS 325
Qy 388 -----PW-----WPDORTACSNHELQLAVENLIV----- 412
Db 326 DFASYQSILDPNNSRNPFREFW-EERFHCSFRQDCAAHSLRAVPFPEQESKIMFVUNA 384
Qy 413 -----STNSIVGNVNVSYSLNNHMFNSQL-----RKQSAQHFQDGFSGGYGPRI 459
Db 395 VYAMAHALNHMRALCPN-----TTHLCDAMPVNGRRLYKDFVLNVKFDAPFP-- 434
Qy 460 IAAQTSDSRRRRRRVVGTSGGHLFPEAISOYAPOTYDAVMAIALARAAEEHRRNEEQ 519
Db 435 -ADTDDEVFRD-----FGDGIGRYNIFTY-----LRAGSGRYRYQKVG 472
Qy 520 SKLGDFTYTRSDMAEFLQMGKHLFLGVSGVPVSFG-----PDRVGTATFYQIORGLL 573
Db 473 YWAEGLTDTSTIPWASPS-----AGPLPASRCEPCLQNEVKSVPQGVCCWLC 522
Qy 574 EPVALYYPATDALDFRCRCRKPWKH---SGQVPYIAKRVFKLRVA-TIAPLAFYTIATL 628
Db 523 IPCQPYEYELD-EFTCADCGLGWPNASLTGCPELPOEYIRWGDWAVGVPV---TIACL 577
Qy 629 SSVGIALATTF-LAFNLHFRKLAIKLSSPKLSNITAVGCCIFVYATVILGLDHSPLSPA 687
Db 578 G----ALATFLVLGVFVRHNATPVWKASGRELCYILLGGVFLCYCMTFFVIAKPSI--- 629
Qy 688 EDSFATVCTARVYLLSAGSLAFSGMFAKYRVRIIP---TRTGSVFKKMLQDIQILLY 745
Db 630 -----AVCTLRRLGLGTAFSVCSYALLTKTNRIARIFGGAREGAQ-RPRFISPASVAIC 683
Qy 746 GGLLVDALLVTLWVYTDPMERHLNLTLEISATDRSVV-YQPOVEVCRSQHTQWLVL 804
Db 684 LALISQILLVAANLV-----VEAPGGKETAPERREVVTLRCNHRDASMLGS 731
Qy 805 YAYKGLLLVGVYMAWETHRVKIPA-LNDISOYIGSVSVSVITSIAVVVLANLISERVTL 863

```

Db      732 LAYNVLLIALCTLYAFKTR--KCPENFNEAKFGFTMYTTCI-----IWL 774
      || ||: : ||: || || ||: || ||: || ||: || ||: || ||: || ||: ||
Qy      864 FTITITALITST-----TATLCL-----LFTPKLHDI 891
      || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
Db      775 AFLPI--FVFTSDYRVQITTCVSVSLGSSVVLGCLFAPKLHI 817
      || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||

RESULT      6
JH0562
metabotropic glutamate receptor 3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C:Accession: JH0562
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:92110002
A:Accession: JH0562
A:Molecule type: mRNA
A:Residues: 1-879 <TAN>
A:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of f
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; trans
F:1-22/Domain: signal sequence #status predicted <SIG> #status predicted <MET>
F:23-87/Proct: metabotropic glutamate receptor 3 #status predicted <TRI>
F:577-599/Domain: transmembrane #status predicted <TRI>
F:614-634/Domain: transmembrane #status predicted <TII>
F:646-664/Domain: transmembrane #status predicted <III>
F:689-709/Domain: transmembrane #status predicted <TIV>
F:735-756/Domain: transmembrane #status predicted <TRV>
F:770-791/Domain: transmembrane #status predicted <TVI>
F:804-828/Domain: transmembrane #status predicted <VII>
F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predi
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

```

Query Match	5.1%	Score 343;	DB 2;	Length 879;
Best Local Similarity	20.1%	Pred. No. 1e-15;		
Matches 200;	Conservative 132;	Mismatches 323;	Indels 340;	Gaps 45;

Qy	151	GKIVLLGLFELS	-----TSRGPRDPGLSELGAATMAVEHINRRK-LLPG-----YTL	196
Db	37	GDVLGGILFINEKGTGTECGGRINEDRGQRLEAMLAFAIDELKNONYLLPGVKLGHVILL	96	
Qy	197	ELVTNDR	-----QCDPGVGVDFEFHAIYQTQSTRVMMLGSA	234
Db	97	DTCSRDTYALBQSLFVRSLSITKVDEAYMCPDG	-----SYAIQNIPLLLAGVIGGSY	150
Qy	235	SEVTESLAKVVPYWNIVQVSGTSPALSDDRRFFPYRTVPADSSHNPARIAFIRKFGW	294	
Db	151	SSVSIQVANLLRLFIQISVASTSAKLSDKSYDFARTVPDPFYQAKAMAEILLRFPNW	210	
Qy	295	GTWTFESONEEVHSLAVNNLVLEAANISCAITIFAATDFKEOL	-----LLLRETDPR	349
Db	211	TYVSTVASEGDYGTGETEAREQEQRJURNICATAEKVGRSNIRKSYDSVIRELLQKPNAR	270	
Qy	350	IIIGSFQELAPQILCBAYRLRMFGADYAMILHESMGA	-----	387
Db	271	VVVLFMRSDDSLIAAANRV	-----NASFTWVSDGNGAQOESIVKSGEHVAYGAITLELAS	327
Qy	388	-----PWPD-----QRTACS-----NH-----ELOLAVE-----	407	
Db	328	HPVRQDFRYFQSLNPYNHNRPNWFRDFWEOKFCQSLQNRHNRHQVCDKHLAIDSSNYEOE	387	
Qy	408	-----NLIVVSTH-----NSIVGNVNVSYGLNNHMFNSOLRKO	-----SAQFHQ	447
Db	388	SKIMFVNNAVYMAHALHKMORTICPNTTKLDAMKILDGKLYEYLLKINFTAPFNPN	447	
Qy	448	DG	-----FGSGYGPRIISAATQSDSRRRRRRGVWGTSG-----GHLFPEAISQY	491
Db	448	KGADSVKEDTFDGGMG-RYVNENLOO	-----TGKYSYLVKGVH-----	485


```
Db 346 PAVPVNKLQDARIILVGLFYETARKVCEVYKERLFGKKYVWFLGWADNWKFIYDP 405
QY 394 RTACSNHLEQLAVENLIVVSTHNSIVGNVNVSYSGLNHMFNSQLRKOSAOPHGDGFGSG 453
Db 406 SINCTVDTEATEAVEGHITTEIVMLNPANTRISINMTSQEFVEKLTK----- 451
QY 454 YGPRISIAATQSDRRRRRRGGVGTGGHLFPEAISOYAPOTYDVAWAIALALRAAEHW 513
Db 452 -----RLKRHPETGG-----FOEAPLAYDAIWAIALALANKTSGGG 487
QY 514 RRNEOSKLDGFDYTRSDMAWEFLQOMKGLHFLGVSPVSF-SGPDRTGVTAFQIQRLG 572
Db 488 GRS--GVRLEDNFNNQITDQIYRAMSSSFEVSGVSHVDFDASGRMANTLIEPOGGGS 545
QY 573 LEPVALIYPATDALDPRCPRPVKWHSGOVPIAKRVFKLRVATIAPIAFYTIATLSSVG 632
Db 546 YRKIGYDSTKDDLSW----SKTDKWTGGSPPADQTLIVIKTRFLSQKLFISVSLSLG 601
QY 633 IALAITFLAFNLHFRKKAIKLSSPKLSNITAVGCCIFVYATVILLGLDHSFLPSAEDSFA 692
Db 602 IIVAVVCLSFNINSHVRVIONSQPNLNLITAVGCSALAAVPLGLDGYHI--GRNOFP 659
QY 693 TVCTARVYLLSAGFSIAFGSMFAKTVYRIFRTGVSFKD-----KMLQDIQILLLVG 746
Db 660 FVQARLWLLGFSIGYSGMFTKIWWHTGFTK-----KEEKWKRTLEPHKLYATVG 714
QY 747 GLLLDVALLVTLWVDPMERHJLHNTLEISATDRSVVYQPOVEVCRSQTHTWLSVLYA 806
Db 715 LLVGMVLTALAIQIWDPLHRTTETAKEPKEDIDVSLPQLEHCSSRKMTWLGIIFYG 774
QY 807 YKGLLLVGVYMAWETHRVHKIPALNDSQYIGVSVSVVITSVAVVLANLISERVTLAFI 866
Db 775 YKGLLLLGIFLAYETKSVSTEKINDHRAVGMAYINAVLCLITAPVTMLSSQDDAFA 834
QY 867 TITAILITSTTATLCLLIPKLDHIWARNDIIDPVHISMGLKMECNRRFVDDRRRELQY 926
Db 835 FASLAIVFSSYITLVLFVFKMRILTRGEWQSEADQTMKTGSTN-----NNEEKS 888
QY 927 RVEVONRVYKKEIQALDAEIRKLERLLES 955
Db 889 LLEKENRELEKIIAEKEERVSELRHQLQS 917
```

```
RESULT 2
T29703
hypoetical protein zk180.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29703
R:Pauley, A.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid zk180.
A:Reference number: Z20669
A:Accession: T29703
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-402 <PAU>
A:Cross-references: EMBL:058748; PIDN:AAB52965.1; GSPDB:GN00022; CESP:zk180.1
A:Experimental source: strain Bristol N2; clone zk180
C:Genetics:
A:Gene: CESP:zk180.1
A:Map position: 4
A:Introns: 25/3; 98/2; 219/3; 253/3; 280/1; 309/1; 339/2; 357/3; 395/2

Query Match 6.4%; Score 429.5; DB 2; Length 402;
Best Local Similarity 33.9%; Pred. No. 2.5e-22;
Matches 103; Conservative 60; Mismatches 104; Indels 37; Gaps 8;
QY 535 EFLQOMKGLHFLGVSPVSGFSDRTGVTAFYQIQRLLEPVALIYPATDALDPRCPRCR 594
Db 11 KMWELDNSSFOGLTGKRVFANNERLGLVDIKQWSDGQYVPFAYDGAAD--EFKIIDST 68
```

```
QY 595 PVKWHSGOVPIAKRVFKLRVATIAPIAFYTIATLSSVGIALAITFLAFNLHFRKKAIAKL 654
Db 69 TKGW---SPLDSTTERRREHIS-----SILFLAMSEL-----IKM 102
QY 655 SSPKLSNITAVGCCIFVYATVILLGLDHSFLPSAEDSFATVCTARVYLLSAGFSIAFGSMF 714
Db 103 SSPNLNIIAGSICTFASVIMGLD--TRIVSPDVFVWLCYTKWTLCIGITLSEFGAMF 160
QY 715 AKTYRVHRIFRTGVSFKD-KMLQDIQILLLVGGLLLDVALLVTLWVDPMERHJLHNT 773
Db 161 SKTVRHSIFT---NIMDRKAIKDSKLFILIGILLIDICVLVWAFVSPFS---YTVT 214
QY 774 LEISATDRSVVYQPOVEVCRSQTHTWLSVLYAYKGLLLVGVYMAWETHRVHKIPALNDS 833
Db 215 ELPHIPEDNIVLIPEVEKCNSSHGVFQAVLYAVXGVLMLGCLFALAWETHRVHNVNVALNDS 274
QY 834 QYIG 837
Db 275 KYIG 278

RESULT 3
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A46742
R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakani
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate recepto
A:Reference number: A46742; MUID:93280152
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NAK>
A:Cross-references: GB:DL13963; NID:g391856; PIDN:BAA03066.1; PID:g391857
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein
```

```
Query Match 5.5%; Score 367; DB 2; Length 871;
Best Local Similarity 21.8%; Pred. No. 2.1e-17;
Matches 189; Conservative 130; Mismatches 361; Indels 188; Gaps 32;
QY 151 GKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLLPG----- 193
Db 31 GGLTLGGLFPVH-ARGAAGRACGALKKEGVHRLEAMLYALDRVNADPELLPVRLGARL 89
QY 194 -----YTLELVNDTQ-----CDPGVGVDRFHAIYTOPSTRMVL 230
Db 90 LDTCSRDTYALEQALSFVQALIRGRGDGEASVRCPGV-----PPLRSAPERVAVV 143
QY 231 GSACSEVTESLAKVYPYNNIVQVSGSTSPALSDRRPEPYFYRTVAPDSSHNPIAFIR 290
Db 144 GASASSVIMVANVLRLFAIPAQISYASTAPELSDTRYDFSRVVPVPPDSYQAQAVDIVR 203
QY 291 KFGCTVTFVTSQNEBVHSLAVNNLV-TELEAANISCAATITFAAT----DFKEQLLLRE 345
Db 204 ALGWNVSTLASEGNYGESGVEAFVQISREAGGVCAIOSIKIPREPKEGFEHKVIRRLME 263
QY 346 TDTRIIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHELOLA 405
Db 264 TPNARGIILFANEDDIRVLEATROANLTGHFLWGSWSGSKISP-----ILNLE 314
QY 406 VENLIVVSTHNSIVGNVNVSYSGLNHMFNSQLRKOSAOPHGDGFGSGVGPRIATAATQS 465
Db 315 EEAVGAI---TILPKRASIDGFDQYFMTSRLENRRNIWFAEFEEFNENFNCNLTSSGGS 370
QY 466 DSRRRRRRGVGTSGGHLFPAISQ---YAPQ-----TYDAWATALALRAAE----- 511
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:06:10 ; Search time 41.85 Seconds
(without alignments)
2375.335 Million cell updates/sec

Title: US-09-715-962-6
Perfect score: 6705
Sequence: 1 MRIIPVQGVTRYGPWPVAVL.....RLSLGDSBEEQQAPANGTE 1305

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*

1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	979.5	14.6	960	2 JE0356	gamma-aminobutyric
2	429.5	6.4	402	2 T29703	hypothetical prote
3	367	5.5	871	2 A46742	metabotropic gluta
4	348.5	5.2	915	2 A49874	metabotropic gluta
5	343.5	5.1	872	2 JH0561	metabotropic gluta
6	343	5.1	879	2 JH0562	metabotropic gluta
7	336.5	5.0	908	2 I49142	metabotropic gluta
8	336	5.0	879	2 JC7160	metabotropic gluta
9	336	5.0	912	2 JH0563	metabotropic gluta
10	306.5	4.6	999	2 T27628	hypothetical prote
11	283.5	4.2	1267	2 T21340	hypothetical prote
12	257.5	3.8	1199	2 A41939	G protein-coupled
13	256	3.8	1171	2 A42916	metabotropic gluta
14	240	3.6	1085	2 S40476	Ca(2+)-sensing rec
15	237	3.5	1078	2 A56715	calcium receptor (
16	233.5	3.5	1088	2 B56715	calcium receptor (
17	224	3.3	1218	2 S71376	glutamate receptor
18	223.5	3.3	1212	2 JC2131	metabotropic gluta
19	221.5	3.3	1079	2 I59362	calcium/polyvalent
20	220.5	3.3	1180	2 JC2132	metabotropic gluta
21	206	3.1	253	2 T29704	hypothetical prote
22	205.5	3.1	976	2 T51137	ionotropic glutama
23	203	3.0	962	2 D86186	hypothetical prote
24	200.5	3.0	941	2 T51135	ligand-gated chann
25	194.5	2.9	898	2 T05099	hypothetical prote
26	191.5	2.9	551	2 T30806	metabotropic gluta
27	180.5	2.7	953	2 E84732	probable ligand-ga
28	179	2.7	920	2 B84640	probable ligand-ga
29	178.5	2.7	1118	2 T27865	hypothetical prote

30 176.5 2.6 950 2 T51134 ionotropic glutama
31 167.5 2.5 934 2 T02742 probable ligand-ga
32 166.5 2.5 921 2 T51136 ionotropic glutama
33 166.5 2.5 923 2 F84732 probable ligand-ga
34 166.5 2.5 1047 1 OYRTHR atrial natriuretic
35 166.5 2.5 1047 2 I45882 C-type natriuretic
36 166 2.5 1112 2 T28082 hypothethical prote
37 165.5 2.5 951 2 T51132 probable glutamate
38 164.5 2.5 925 2 T51133 ligand gated chann
39 164.5 2.5 975 2 A84550 probable ligand-ga
40 163 2.4 912 2 T51131 ligand gated chann
41 162.5 2.4 1047 1 OYHUBR natriuretic peptid
42 160 2.4 847 2 T34577 probable export pr
43 160 2.4 925 2 T06128 hypothethical prote
44 155.5 2.3 938 2 T01809 hypothethical prote
45 155 2.3 454 2 S75741 hypothethical prote

ALIGNMENTS

RESULT 1
JE0356
gamma-aminobutyric acid receptor B precursor - human
N:Alternate names: GABA(B) receptor
C:Species: Homo sapiens (man)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 12-Feb-1999
C:Accession: JE0356
R:Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante
Biochem. Biophys. Res. Commun. 250, 240-245, 1998
A:Title: GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine m
A:Reference number: JE0356; MUID:98440782
A:Accession: JE0356
A:Molecule type: mRNA
A:Residues: 1-960 <GRI>
A:Cross-references: GB:Y11044; NID:2826760
A:Note: this ORF is not annotated in GenBank entry HSGTHLAL, release 109
C:Genetics:
A:Map position: 6p21.3-6p21.3
C:Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:1-960/Domain: signal sequence #status predicted <SIG>
F:12-960/Product: gamma-aminobutyric acid receptor B #status predicted <MAT>
F:590-613/Domain: transmembrane #status predicted <TM1>
F:527-654/Domain: transmembrane #status predicted <TM2>
F:566-687/Domain: transmembrane #status predicted <TM3>
F:709-730/Domain: transmembrane #status predicted <TM4>
F:767-788/Domain: transmembrane #status predicted <TM5>
F:803-825/Domain: transmembrane #status predicted <TM6>
F:831-856/Domain: transmembrane #status predicted <TM7>
F:23,83,439,481,501,513,630/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 14.6%; Score 979.5; DB 2; Length 960;
Best Local Similarity 29.6%; Pred. No. 2.5e-60;
Matches 257; Conservative 155; Mismatches 364; Indels 93; Gaps 17;
QY 100 RLNSHNLPGSTWASHAHLNLPQRQYLKVNQVFESERMSPAEMORNGKIVLLGLF 159
DB 129 RCDPDFHLVGSRRSICSGQWSTP--KPHCQVNRTPHSRR-----AVYIGALF 175
QY 160 ELSTSRGPRDGLSELGAATMAVSHINKR--LLPGYTELVNTDQDPGVGVDRFFHAI 218
DB 176 PMS---GGWPGGQACQPAVEMALDVNSRRDILPDYELKLIHDSKCDPGQATKLYELL 232
QY 219 YTOPSTRMWMLLGSSEVTESLAKVVPYWNIVQVSGSTSPALSDRREFPYFRTVAPD 278
DB 233 YNDP---IKIILMPGCCSVSTLVAEARMNLIIVLSGSSSPALSNQRFFFTFTHPSA 289
QY 279 SSINPARIARFPGWGTVTTFSSQNEVHSLAVNVLVTELAANISCAATTFATDPEKE 338
DB 290 TLNHPTRVKLFKQWGWKKIATIQOTTEVFTSLDLEERVKEAGIE----ITFROSFFSD 345
QY 339 QLL---LLRETDRFIIIGSFSQELAPQILCEAYRLRMEGADYAWILHESMGAPWMP---DQ 393

```
FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 452 452 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 555 555 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 893 908 TSSTKTYISYNSHSI -> SKSSVEFFPMVKGSGTS (IN ISOFORM B).
FT VARSPLIC 454 501 SAGTPTFNENGADPGRYDIFQYITNKSPSYKVGHWITNO
LHLKVED -> CRRGIOMSLPWTLTPTSPSSWAVLALLS
LMLKTEMLDVMISSIK (IN ISOFORM C).
FT VARSPLIC 502 908 MISSING (IN ISOFORM C).
FT CONFLICT 194 194 R -> A (IN REF. 2).
FT CONFLICT 460 460 T -> I (IN REF. 2).
FT CONFLICT 642 642 A -> G (IN REF. 2).
FT CONFLICT 768 768 I -> N (IN REF. 1).
FT CONFLICT 904 904 S -> T (IN REF. 2).
SQ SEQUENCE 908 AA; 101740 MW; 95C2D5883DAF6FDE CRC64;

Query Match 5.0%; Score 337.5; DB 1; Length 908;
Best Local Similarity 20.7%; Pred No. 1.2e-15;
Matches 207; Conservative 153; Mismatches 339; Indels 301; Gaps 46;

Qy 146 MORNH-----GKIVLLGLFELST--SRG-----PRPDGLSELGAATMAVEHIN 186
Db 28 MORTHQEYAHISIRVDGDIILGLFPVHAKGERGVPCEGLKKEKIHLEAMLYAIDQIN 87
Qy 187 R-KRLLPGYTL-----ELVNDTQC---DPGVGVDRFFH 216
Db 88 KDPDLLSNITLGLVRILDTCSRDTYALEQSLTFVQALIEKDASDVKANGDP----- 138
Qy 217 AIYTOPSTRMVMMLGSACSEVTESLAKVYPMNIVOVSGSTSPALSDRREFFPYRTVA 276
Db 139 PIFTRPD-KISGVIGAAASVSIMANILRLKIPOLISTASTAPELSDNTRYDFFSRVP 197
Qy 277 PDSSINPARIARIRFGWGTVTTFSON---EEVHSLAVNNLVTELEAANISCAATITFAA 333
Db 198 PDSYQAQAVDIVTALGNWYVSTLASEGNYGESGVEAFTQISREIGGVCIASQOKIPREP 257
Qy 334 T--DFKEQLLLRET-DTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMG---A 387
Db 258 RPGEFEKIKRLLETPNARAVINFANEDIRILEAAKKLNQSG-HFLWIGSDSWGSKIA 316
Qy 388 PWMPOQTACSNHELQAVENLIVVSTHNSIVGNVNNYSYGLNNH-----MFNSQLRKQA 442
Db 317 PYQOEET-----EGAV-----TILPKRASIDGDFRYFRSRTLANNRRNWF 360
Qy 443 QFHGDGFGC---SGYGPRIISAATQSDRRRRRGVGTSGGHLFPEAISQYAPQTYDVA 499
Db 361 EF-WEENFGCKLGGHGRNSHIKKTGLERIARDSSYEQEGKVQF-----VIDAV 409
Qy 500 WAIALALRAAEHHRNE-----BQSKLDGFDYTRSDMAWEFLQOMKGLHFLGVS 549
Db 410 YSMAYAL-----HNMHKDLCPGYIGLCPRMSTIDG-----KELGYIRAVNNGSA 455
Qy 550 G-PVSFS-GPDRVGTATFQIQ-----RGLLEPVAL 578
Db 456 GTPVTFNENGADPGRYDIFQYITNKSTEYKVGHWITNQLHLKVEDMQWAHREHTHPASV 515
Qy 579 -----YYPATDALDFRCPC-----RP----- 595
Db 516 CSLPCKPGERKTVKGVPCWCERCCEGNYQVDELS--CELCPLDQRPNNMTGCOLIP 573
Qy 596 ---VKWHS--GOVPIAKRVKRLVATIAFLAFYTTATLSSVGIALAITFLAFNLHFRKLK 650
Db 574 IKLEWHSPWAVVPVAILGIATTF-----VIVTFVRYN---DTP 612
Qy 651 AIKLSPLKSNITAVGCIFVYATVILLGLDHDSTLPSAEDSFATVCTARVYLLSAGFSLAF 710
Db 613 IVRASGRELSVYLLAGIFLCYSITEL-----MTAAPDTI--ICSFRRVFLGLGMCFSY 663
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Qy 711 GSMFAKTYRVHRIFTR-TGSVFQKMKMLQDIQLILLVGGLLLDALLVTLVWVTDP----- 764
Db 664 AALLTKTNRIHRIFFQGGKKSVTAPKFISPASQLVITFSLISVOLLGVFMVFMVVDPPHII 723
Qy 765 -----MERHLNLTLEISATDRSVVYQPOVEVCBSQHTQTWLSVLYAYKGLLLVGVY 817
Db 724 DYGEQRTLDPEKARGVLKCDISDLSL-----ICS-----LGSILLMVTCTV 765
Qy 818 MAWETRHRVKIPALNDSQYIGSVSVY-VITSAIVVVLNLI--SERVTLAFITITALILT 874
Db 766 YAIKTRGVP-ETFEAKPIGFTMYTCIIWLAFIPFIFFGTQAQSAEKMYIQTTTLTVMSML 824
Qy 875 STTATLCLLFIPLKLDIWARNDIIDPVIHSMGLKMECNTRRFVVDRELOQYAVEV--- 930
Db 825 SASVSLGMLYMPKVYII-----IFHP-----BQNVQ-----KKRSEKAVVTAAT 864
Qy 931 -QNRVYKKEIQALDAEIRKLERLLESGLTTTSTTTSSSTS 969
Db 865 MOSKLIQKGNDRPNGEVK--SELCESETNTSSTKTYIS 902
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Search completed: April 30, 2002, 10:08:14
Job time: 201 sec

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Db 139 PIFKPD-KISGVIGAAASSYIMVANILRLFKIPQISYASTAPELSDNTRDYDFSRVVP 197
QY 277 PDSSHNPARIAFIRKFGWGTVTTSQNF--BEVHSLAVNNLVTELEAANISCAATITFAA 333
Db 198 PDSYQAQMDIVTALGWNYSVTLASSENGYSGVEAFTQISREIGGVCVIAQSQKIPREP 257
QY 334 T--DFKQLLLRET-DTRIIGSFSQELAPQICEAFLRMFGADYAWILHESMG---A 387
Db 258 RPGEFEKILRLLETPNARAVIMFANEDDIRLEAAKLNQSG-HFLWIGSDSWGSKTA 316
QY 388 PWNPDQRTACSNHELQLAVALNVLVSTHNSIVGNVSYGLNNH-----MENSQLRKQSA 442
Db 317 PVQOEIA-----EGAV-----TILPKASIDGDFRYFRSRTLANNRRNVWFA 360
QY 443 QFHGQDGF-----SGYGRISIAATQSDRRRRRGVGTSGHLEPPEAISQYAPQTYDAV 499
Db 361 EF-WEENFGCKLGHGRNSHKIKTGLERTARDSSYEQEGKVQF-----VIDAV 409
QY 500 WAIALALRAAEHWRNEEQSKLDFYTRSDMAW-----EFLQMGKHLFLVSG-PVSF 554
Db 410 YSMAYAL-----HNMHKERCPCYIGLCPRMVTIDGKELLYIRAVNFGSAGTPVTF 461
QY 555 S-GPDRVGTTFAYQIQ-----RGLLEPVAL-----578
Db 462 NENGDAFGRYDIFQIINKSTYKIIQHTWNLHLKVEDQMANKREHTHPASVCSLPCK 521
QY 579 -----YYPATDALDFRCPRC-----RP-----VKW 598
Db 522 PGERKKTGVPCWCHERCCEGYNQVDELS--CELCPDQRPINRGTQCORIPIKLEW 579
QY 599 HS--GVQPIAKRVKPLRVATIAPIAFYTIATLSSVGIATFTLAFNLHFRKLKAIKLS 656
Db 580 HSPWAVVVFVAILGIIATTF-----VIVTFVRYN-----DTPIVRASG 618
QY 657 PKLSNITAVGICFYVATVILGLDHLSTLPSAEDSFATVCTARVYLLSAGFSIAFGSMFAK 716
Db 619 RELSYVLTGLFLCYSTFL-----MIAAPDTI--ICSFRIIFGLGCMFSYAALLTK 669
QY 717 TYRVHRIFR--TGSVFKDKMLQDIQIILLVGLLLVDALLVTLVWVTPDPMERHLNLTLE 775
Db 670 TNRIHIFEQCKSVTAPKFSIPASQVITFSLISVQLLVGVFVWVDPHP-----TII 723
QY 776 ISATDRSVVYQPOVECRSQHTQWLSVLYAYKGLLLVGVVYMAWETHRVHKVIALNDSOY 835
Db 724 DYGEQRTLDPENARGVLKCDISLCSGLYSILLMTCTVYIAIKTRGVP-ETEFNEAKP 782
QY 836 IGVSVYSV-VITSAIVVVLNLI--SERVTLAFITITLITLTSTATLCLLFIPLKLDIW 892
Db 783 IGFTMTTCIIWLAFIPIFFGTQAQSAEKMYIQTTLTVSMLSUSASVSLGMLYMPKVYIII- 841
QY 893 ARNDIIDPVIHSMGLIKMECNTRRFVVDORRELQYRVEV-----QNRVYKKEIQALDAETR 947
Db 842 -----IFHP-----EQNVQ-----KRRSFRAVTAATMQSKLIKQGNDRPNGEVK 882
QY 948 KLERLESGLTTTSTTSSTSSVS 969
Db 883 --SELCSLETNSTSTKTYIS 902

RESULT 15
MGR8_HUMAN
ID MGR8_HUMAN STANDARD; PRT: 908 AA.
AC O00222; O15493; O95945; O95946;
DT 01-NOV-1997 (Rel. 35, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

```

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RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rostock P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells."
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=97446143; PubMed=9299241;
RA Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.-C.;
RT "The human metabotropic glutamate receptor 8 (GRM8) gene: a
RT disproportionately large gene located at 7q31.3-q32.1."
RL Genomics 44:232-236(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C).
RC TISSUE=Fetal brain;
RA Malherbe P., Kratzeisen C., Lundstrom K., Richards J.G., Faull R.L.M.,
RA Mutel V.;
RT "Cloning and functional expression of alternative spliced variants of
RT the human metabotropic glutamate receptor 8."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
EMBL: U92459; AAB51764.1; -
EMBL: U95025; AAB72040.1; -
EMBL: AJ236921; CAB36968.1; -
EMBL: AJ236922; CAB36969.1; -
DR GCRDB; GCR_1889; -
DR GCRDB; GCR_2604; -
DR MIM: 601116; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01058; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction; Alternative splicing.
FT SIGNAL 1
FT CHAIN 34
FT DOMAIN 34 583
FT TRANSMEM 584 608
FT DOMAIN 609 620
FT TRANSMEM 621 641
FT DOMAIN 642 647
FT TRANSMEM 648 668
FT DOMAIN 669 695
FT TRANSMEM 696 716
FT DOMAIN 717 746
FT TRANSMEM 747 768
FT DOMAIN 769 781
FT TRANSMEM 782 803

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Db 210 VASEGDVETGIEAEAEARARNI-CVATSEKVGGRAMSAEFGVVRRALLQPSARVAVL 268
QY 354 SFSQELAPQIICEAYRLRMFGADYAWILHESMGA----- 387
Db 269 FTRSEDARELLAQTORL---NASFTWASDGMGALSVVAGSERAAGAITIELASYPIS 325
QY 388 -----PW-----WPDQRTACSNHQLQAVENLIV----- 412
Db 326 DFASYFOSLDPNWNSRNPWFREFW-EERFHGCSFRORDCAAAHSLRAVPFPEQESKIMFVNA 384
QY 413 -----SPHNSITGVNNVSYSLNNHNSQL-----RKQSAQFHGQDGFSGVGPRTS 459
Db 385 VYAMAHALNNHRRALCPN-----TTHLCDAMRVNRRLLKYKDEVNLNVKFDAPFRP----- 434
QY 460 IAATQSDSRRRRRRGVGTSGHLPPEAISQVAPOTYDAVMAIALARAAEEHWRNNEEQ 519
Db 435 -ADTDDEVRFDR-----FGDGRVNYITY-----LRAGSGRYRQKVG 472
QY 520 SKLGDGYTRSDMAWEFLQOMKHLFLVSGVPVSFG-----PDRVGTATFYQIQRL 573
Db 473 YWABGLTLDTSFIPWASPS-----AGPLPASRCSEPCIQNEVKSVPQGEVCCWLC 522
QY 574 EPVALYYPATDALDPCRCRPVKWH-----SCQVPIAKRVFKLVA-TIAPLAFYTIATL 628
Db 523 IPCOPYEYRLD--EFTCADCLGVWPNASLTGCFELPOEYIRWGDAWAGVPV---TIACL 577
QY 629 SSVGIALAITE-LAFNLHFRKLKALKSPKLSNITAVGCIIFYATVILLGLDHSFLPSA 687
Db 578 G-----ALATFLVGVFVRHNPVVKASGRELICYLLGGVFLCYCMTFVFIKPSI----- 629
QY 688 EDSFATVCTARVYLLSAGFSIAFGSMFAKTYRVHRIF--TRTGSVFKMKMLQDIQLILV 745
Db 630 -----AVCTLRRLGLGTAFSCVYALLTKTNRIARIFGAREGAQ-RPRFISPASQVAIC 683
QY 746 GGLLDVALLVTLVWVTPMERHLNHLNLEISATDRSVV-YQPOVEVCRSHQTOHLSVL 804
Db 684 LALISGQLLIYAAMLV-----VEAPGTGKETAPERREVVVTLRCNHRDASMLGS 731
QY 805 YAYGKLLLVGVWYAWETRRHKIPA-LNDSOVIGVSVSWITSATVVVLANLISERVTL 863
Db 732 LAYNVLLIALCTLYAFKTR--KCPENFNEAKFIGHTMYTTCI-----IWL 774
QY 864 AFITITALLFST-----TATLCL-----LFTPKLHDI 891
Db 775 AFLPI--FYVTSSDYRVQTTMCSVSVSLSGSVLGGVLCGLFAPKLHII 817

RESULT 13
MGR3_RAT
ID MGR3_RAT STANDARD; PRT; 879 AA.
AC P31422;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PRECURSOR.
GN GRM3 OR GPRC1C OR MGLUR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92110002; PubMed=1309649;
RA Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi S.;
RT "A family of metabotropic glutamate receptors.";
RL Neuron 8:169-179(1992).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINANT

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CC EXPRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
CC DENTATE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR2.
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CC EMBL; M92076; -; NOT_ANNOTATED_CDS.
CC PIR; JH0562; GCR_0362;
CC GCRDB; GCR_0362;
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC PRINTS; PR00248; GPCRMRG.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01053; MTABOTROPIC3R.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family.
CC SIGNAL 1 22 POTENTIAL.
CC CHAIN 23 879 METABOTROPIC GLUTAMATE RECEPTOR 3.
CC DOMAIN 23 576 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 577 599 I (POTENTIAL).
CC DOMAIN 600 613 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 614 634 II (POTENTIAL).
CC DOMAIN 635 645 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 646 664 III (POTENTIAL).
CC DOMAIN 665 688 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 689 709 IV (POTENTIAL).
CC DOMAIN 710 734 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 735 756 V (POTENTIAL).
CC DOMAIN 757 769 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 770 792 VI (POTENTIAL).
CC DOMAIN 793 802 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 803 828 VII (POTENTIAL).
CC DOMAIN 829 879 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 414 414 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 439 439 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 879 AA; 98959 MW; 3E5965EDD5E6DEED CRC64;

Query Match 5.1%; Score 343; DB 1; Length 879;
Best Local Similarity 20.1%; Pred. No. 4.5e-16;
Matches 200; Conservative 132; Mismatches 323; Indels 340; Gaps 45;

QY 151 GKIVLIGLGFELS-----TSRGRPRDGLSELGAATWAVEHINRKR-LLPQ-----YTL 196
Db 37 GDVLVGLGFLPINEKGTGTEECGRINEDRGIORLEAMLFAIDINKDNTLLPGVKVGLVHIL 96
QY 197 ELVTNDT-----QCDPGVGVDVFHAIYTOPSTRVMVLISGAS 234
Db 97 DTCSDRYALQSLFVFRASLTKVDEAYMCPDG-----SYAIGENPLLIAGVIGSY 150
QY 235 SEVTESLAKVVPYNNIVQVSGSTSPALSDRRPEFYRTVAPDSSHNPARTAFIRKFGW 294
Db 151 SSVSIQVANLLRLFIQIPQISVASTSAKLSKDSRYDYFARTVPPDFYQAKAMAEILRFENW 210
QY 295 GTVTTFFSNEEVHSLAVNNLVTELEAANISCAATTTFAATPFKEQL-----LLLRETDTR 349
Db 211 TVSTVASEGDTGETGIEAFQEARLRNICIATAEKVGRSNIRKSYDSYVIRELLQPNAR 270

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CC -1- TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT
CC EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME
CC PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR3.
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FT DOMAIN      820   872   CYTOPLASMIC (POTENTIAL) .
FT CARBOHYD    203   203   N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD    286   286   N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD    338   338   N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD    402   402   N-LINKED (GLCNAC. .) (POTENTIAL) .
FT CARBOHYD    547   547   N-LINKED (GLCNAC. .) (POTENTIAL) .
SQ SEQUENCE    872 AA; 95773 MW; 1E74CABD6AD4BED9 CRC64;

Query Match          5.1%; Score 343.5; DB 1; Length 872;
Best Local Similarity 21.6%; Pred. No. 4.1e-16;
Matches 191; Conservative 115; Mismatches 338; Indels 241; Gaps 36;

QY 151 GTKVLGFLFELSTSRGRPD-----GLSELGAATMAVEHINR-KRLLPG----- 193
   | :| | | | :| | :| :| :| | | | |
Db 30 GDVLGGLFPVHKGGPAECGPGNEHRGIQRLEAMLFALDRINRDPHLLPGVRLGAHIL 89

QY 194 -----YTLELVNTDTQCDPGVGVDRFFH-----AIYQTPTRMVMLLGSACSSEVTE 239
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 90 DSCSKDTHALEQALDFVRASLRSGAGCSRRICPDGVSATHSDAPTAVTGVIGGYSYDSVI 149

QY 240 SLAKVPYPWNIVQVSGSTSPALSDREFFPYFFYRTVAPODSSHNPARTAFTRKKGWGTVTT 299
   | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 150 QVANLLRFQIPQISYASTSKSDKSRYDYFARTPEPDFQAKAMAEIILRNWTYVST 209

QY 300 FSONEEVHSIAVNNLVTELEAANISCAATI-----TFAATDFEOL-LLRETDDTRIIG 353
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QY 565 FYQIQ-----RGL-----572
Db 479 IFQIQTNWTPNGVRLICQWDELQNLIEDQMKGVRIPSSVCTLPCKPQGRKTKQG 538
QY 573 -----LEPVALYXPATDALDFRCPRC-----RPVWHSG--OVPIAKRVFKLRVATIAPL 620
Db 539 TPCWCTCEPCDGYQYQFD--EWTQHCYDQDPNENRTGCQNIPIKLEWHSPWVIP--594
QY 621 AFYTIALSSVGIAlAIFLAFNLHFRKLKAIKLSPLKSNITAGVCIFYATVILLGLD 680
Db 595 -----VFLAMGLIITAFVMTAFIRYNDTPIVRASGRELSVLLTGIFLCYIITFLM---646
QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSLAQSMFAKTYRVHRIFTR--TGSVPKDKMLQDI 739
Db 647 -----IAKPDVA--VCSFRFVFLGLGMCISYAALLKTNRIYRIFEQGKKSVTAPRLISPT 700
QY 740 QLILLVGLLLVDALLVTLWVTPDMERHLNLTLEISATDRSVVYQPOVE--VCRSQHT 797
Db 701 SOLAITSLSISVOLLGVFIWGVDP-----PNIIDY---DEHKTWNPQARGVLKCDIT 752
QY 798 QTWLSVLYAYKGLLLVGVYMAWETRRHKIPALNDSQVIGSVYSV-VITSAlVVVYLANL 856
Db 753 DLQICSLGYSILLMVTCTVYAIKTRGP-ENFNEAKPIGETMYTTCIVWLAFIPIFEET 811
QY 857 I--SERVTLAFITITALLITSTATLCLLFPKLHDI 891
Db 812 AQSAEKLYIQTTTLTISMNLSASVALGLMYPKVYII 848

RESULT 11
MGR4_HUMAN
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Insectivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=96346635; PubMed=8738157;
RA Makoff A., Lelchuk R., Oxer M., Harrington K., Emson P.;
RT "Molecular characterization and localization of human metabotropic
RL glutamate receptor type 4.";
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
[2]
SEQUENCE FROM N.A.
MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Ruckey P.K., Burgett S.G., Arnold J.S.,
RA Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RL pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
[3]
SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=95342351; PubMed=7617140;
RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Knoepfel T., Kuhn R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4.";
RL Neuropharmacology 34:149-155(1995).
RL
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.

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CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X80818; CAA56784.1; -.
CC EMBL; U92457; AAB51762.1; -.
CC GCRDB; GCR1891; -.
CC GCRDB; GCR2069; -.
CC MTM; 604100; -.
CC InterPro; IPR001828; ANF_receptor.
CC InterPro; IPR000337; GPCR_Mgr.
CC Pfam; PF00003; 7tm_3; 1.
CC PRINTS; PR001094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01054; MTABOTROPIC4R.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32
FT CHAIN 33 912
FT DOMAIN 33 587
FT TRANSMEM 588 610
FT DOMAIN 611 624
FT TRANSMEM 625 645
FT DOMAIN 646 656
FT TRANSMEM 657 675
FT DOMAIN 676 699
FT TRANSMEM 700 720
FT DOMAIN 721 750
FT TRANSMEM 751 772
FT DOMAIN 773 785
FT TRANSMEM 786 808
FT DOMAIN 809 821
FT TRANSMEM 822 847
FT DOMAIN 848 912
FT CARBOHYD 98 98
FT CARBOHYD 301 301
FT CARBOHYD 454 454
FT CARBOHYD 484 484
FT CARBOHYD 569 569
FT SEQUENCE 912 AA; 101867 MW; 4A2F36B63A2EAF5A CRC64;
QY 148 RNHGKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLPLPYTLE 197
Db 44 RIDGDITLGLFPVH-GRGSGKPCGELKKEGTHRLEAMFLALDRINDDPLLNITLG 102
QY 198 LVTVNDTCDCPGVGVDRFFHA-----CSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITRKE-RWVGVI 230
Db 103 ARILDT-----CSRDTHALEQSLTFVQALIEKDGTEVRCGSGGPPITRKE-RWVGVI 154
QY 231 GSACSEVTESLAKVVPVWNIQVSGFSGSPALSDREFFYFRTVAPDSSHPARIATIR 290
Db 155 GASGSSVIMVANTLRLFKIPQISYASTPDLNSRSDYDFSRVPSDTYQAQAMVDIVR 214
QY 291 KFGWGTVTTFSSQNEEVHSLAVNNLVTE-LEAANISCAATITF-----AATDFKEQLLLRE 345

```

Query Match 5.2%; Score 347; DB 1; Length 912;
 Best Local Similarity 22.5%; Pred No. 2.5e-16;
 Matches 197; Conservative 137; Mismatches 337; Indels 204; Gaps 39;

QY 621 AFVTIATLSSVGTALAITFLAENLHFKLKAIKLSSPKLSNITAVGCIFFVYATVILLGLD 680
 Db 595 -----VFLAMGLIAIFNATIRNDTPIVRASGRELSVLTGLCYITFLM--- 646
 QY 681 HSTLPSAEDSFATVCTARVYLLSAGFSFARQYRHRIFTR-TGSVFKDKMLQDI 739
 Db 647 -----IAKPDVA-VCSFRRVFLGLGMCISYAALLTKTNRIYRIFEQCKSVTAPRLISPT 700
 QY 740 QLILLVGGLLLDVALLVTWVTDPMERHUNLTLAISATDSRSVYQPOVE--VCRSQHT 797
 Db 701 SOLAITSSISVOLLGVFIWFGVDP-----PNIIDY---DEHKTMNPEQARGVLKCDIT 752
 QY 798 QTWLSVLYAVKGLLLVGVYMANETHVKIPALNDSQYIGVSYSV-VITSIVVVLANL 856
 Db 753 DLOICSLGYSILLMTCTVYAIKRGVP-ENFNEAKPIGTMYTTCIVMLAFIPIFGT 811
 QY 857 I--SERVTLAFITITAILTSTTATLCLLPIPKLHDI 891
 Db 812 AQSAEKLYITTLTSMNLASVALGMLYMPKVYII 848
 RESULT 10
 MGR7_RAT STANDARD; PRT; 915 AA.
 AC P35400;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
 GN GRM7 OR GPRC1G OR MGLUR7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94117433; PubMed=8288585;
 RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
 RA Mizuno N., Nakanishi S.;
 RT "Molecular characterization of a new metabotropic glutamate receptor
 RT mGluR7 coupled to inhibitory cyclic AMP signal transduction.";
 RL J. Biol. Chem. 269:1231-1236(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
 RX MEDLINE=94195260; PubMed=8145723;
 RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
 RA Westbrook G.L.;
 RT "Cloning and expression of a new member of the L-2-amino-4-
 RT phosphonobutyric acid-sensitive class of metabotropic glutamate
 RT receptors.";
 RL Mol. Pharmacol. 45:367-372(1994).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.

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 or send an email to license@sib-sib.ch).

 CC EMBL: D16817; BAA04092.1; -;
 CC EMBL: U06832; AAA20655.1; -;
 DR GCRDb; GCR_0945; -;
 DR GCRDb; GCR_0946; -;

DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000337; GPCR_Mgr.
 DR Pfam: PF00003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRMR.
 DR PRINTS: PR00593; MTABOTROPICR.
 DR PRINTS: PR01057; MTABOTROPICR.
 DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
 DR PROSITE: PS02059; G_PROTEIN_RECEP_F3_4; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Olfaction.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
 FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 591 615 I (POTENTIAL).
 FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 628 648 II (POTENTIAL).
 FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 655 675 III (POTENTIAL).
 FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 703 723 IV (POTENTIAL).
 FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 754 775 V (POTENTIAL).
 FT DOMAIN 776 788 VI (POTENTIAL).
 FT TRANSMEM 789 810 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 811 825 VII (POTENTIAL).
 FT TRANSMEM 826 850 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 851 915 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 458 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 486 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 572 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 915 AA; 102231 MW; F28AFC4C6454A6C2 CRC64;
 Query Match 5.2%; Score 348.5; DB 1; Length 915;
 Best Local Similarity 20.4%; Pred. No. 2e-16;
 Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;
 QY 148 RNHGKIVLLGPELSTSRGP-----RPDGLSELGAATMAVEHINR-KRLPGYTL- 196
 Db 44 RIEGDVTILGGLFPVH-AKGPSGVPCGDKRENGIHRLEAMLYALDQINSDPLNPVTLG 102
 QY 197 -----ELVTNDTCQDPGVGVDRFFHAIYTOPSTRMVLG 231
 Db 103 ARILDCSRDYYALEQSLTFVQALLQKDTSDVRNCE-----PPVFKPE-KVGVIG 155
 QY 232 SACSEVTESLAKVPYWNIVQVSFGSTSPALSDRRREFFYRTVAPDSSHNPARIATIRK 291
 Db 156 ASGSSVSIWVANILRLFOIPQISYASTAPELSDRRYDFSRVVPDPSQAQAMDIVKA 215
 QY 292 FGWGTVTFTFSONEEVHSLAVNNLVTLEAANTSCAATITFAATDFKEQLL-----LL 343
 Db 216 LGWNYVSTLASSEGSYGERGVESFTQISKEAGGLCIAQSVRIQERKDRITDFRIKQLL 275
 QY 344 RETDRIIIGFSQELAPQILCEAYLRMFGADYAWILHESMGAPWPDORTACSNHELO 403
 Db 276 DTPNSRAVVIIFANDEDIKOILAAAKRADQVG-HFLWVGSDSWGSKINP-----LHQHE 327
 QY 404 LAVENLIVVSTHNSIVGNVSYGLNNHMFNSQLARKSQAQFHGQDGSYGGYPRISIAAT 463
 Db 328 DIAEGAITIQKRAIV-----EGFDAFTSRTLENNRNWVFAEYWEENFNCKLTISGS 381
 QY 464 QSDSRRRRRRGVGTSGGHLFPPEAI---SQYAPQ-----TYDAVMAIALALRAAEHWR 515
 Db 382 KKEDTDKCTG-----QERIGKDSNYEQEGKGVQFVIDAVYMAHAL-----HMMNK 427
 QY 516 N-----EEQSKLDGDFDTRSDMAWEFLQOMKGLHFLVSG-PVSFS-GPDVGTGA 564
 Db 428 DLCADYRGVCPMEQAGG-----KKLLKYIRHVNFGSAGTPVMFNKNGDAPGRYD 478

Db 688 SGQLLIVAVLV-----VEAPGTGKETAPERREVVTLCNRHDSMLGSLAYN 735

QY 809 GLLLVGVYMAWETRHVKIPA-LNDSQYIGVSVSWITSIAIVVLVLANLISERVTLAFTT 867

Db 736 VLLIALCTLVAFNTR--KCPENFNEAKFETGFTMYTTCIIWLALLPIFYVTSDDYRVQTTT 793

QY 868 ITALILSTTATICTLFFIPKLHDI 891

Db 794 MCVSVLSGVSGLFAPKLHII 817

RESULT 9

MGR7_HUMAN

ID MGR7_HUMAN STANDARD; PRT; 915 AA.

AC Q14831;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.

GN GRM7 OR GPRC1G OR MGLUR7.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=96437220; PubMed=8840028;

RA Makoff A., Pilling C., Harrington K., Enson P.;

RT "Human metabotropic glutamate receptor type 7: molecular cloning and

RT mRNA distribution in the CNS.;"

RL Brain Res. Mol. Brain Res. 40:165-170(1996).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=98141892; PubMed=9473604;

RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,

RA Rostek P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.;

RT "Group III human metabotropic glutamate receptors 4, 7 and 8:

RT molecular cloning, functional expression, and comparison of

RT pharmacological properties in RGT cells.;"

RL Brain Res. Mol. Brain Res. 53:88-97(1998).

CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR

CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE

CC ACTIVITY.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY AREAS OF THE BRAIN.

CC ESPECIALLY IN THE CEREBRAL CORTEX, HIPPOCAMPUS, AND CEREBELLUM.

CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

CC STRONGEST, TO MGLUR4.

CC -----

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CC -----

CC EMBL; X94552; CAA64245.1; -

DR EMBL; U92456; AAB51763.1; -

DR GCRDB; GCR_1890; -

DR GCRDB; GCR_2071; -

DR MTM; 604101; -

DR InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCRMR.

DR PRINTS; PR00593; MTABOTROPICR.

DR PRINTS; PR01057; MTABOTROPICR.

DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Multigene family; Olfaction; Polymorphism.

FT SIGNAL 1 32

FT CHAIN 33 915

FT DOMAIN 33 590

FT TRANSMEM 591 615

FT DOMAIN 616 627

FT TRANSMEM 628 648

FT DOMAIN 649 654

FT TRANSMEM 655 675

FT DOMAIN 676 702

FT TRANSMEM 703 723

FT DOMAIN 724 753

FT TRANSMEM 754 775

FT DOMAIN 776 788

FT TRANSMEM 789 810

FT DOMAIN 811 825

FT TRANSMEM 826 850

FT DOMAIN 851 915

FT CARBOHYD 98 98

FT CARBOHYD 458 458

FT CARBOHYD 486 486

FT CARBOHYD 572 572

FT VARIANT 433 433

FT Y -> F.

SQ SEQUENCE 915 AA; 102250 MW; CFF94E06BF7F4919 CRC64;

Query Match 5.2%; Score 349.5; DB 1; Length 915;

Best Local Similarity 20.4%; Pred. No. 1.7e-16;

Matches 179; Conservative 146; Mismatches 347; Indels 205; Gaps 33;

QY 148 RNECKIVLLGLFELSTSRGP-----RPDGLSELGAATMAVEHINR-KRLIPGYTL- 196

Db 44 RIEGDVTLGGLFPVH-ARGPSGVPCGDIKRENGIHRLLEAMLYALDQINSDNPLPNVTLG 102

QY 197 -----ELVNTDTCQDPGVGVDRFFHAIYQTQSTRMVLG 231

Db 103 ARILDTCSRDTYALEQSILTFVQALIQDTSVRCNCE-----PPVFVKPE-KVGVIG 155

QY 232 SACEVTESLAKVVPYWNIVQVSGTSPALSDRRPPFYRTVAPDSHNPARIATFRK 291

Db 156 ASGSSIMVANIILRFQIPQISYASTAPELSDDRYDFRSRVPPDPFQAQAMVDIVKA 215

QY 292 FGGTGVTFESQNEEVHSLAVNVLVTELEAANISCAATITFAATDFKEOLL-----LL 343

Db 216 LGWNVSTLSEGSYGEGKGVESFTQISKEAGGLCIAOSVRIPQERKRDITDFDRIIKOLL 275

QY 344 RETDTRIIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWPDQRTACSNHELQ 403

Db 276 DTPNSRAVIVFANDEDIKQILAAAKRADQVG-HFLWGSDSMGSKINP-----LHQHE 327

QY 404 LAVENLIVSTHNSIVGNVSYGLNNHMFNSQLRKQSAQFHGQDGFSGYGPRTISIAAT 463

Db 328 DIAEGAITIQKRAIV-----EGFDAYFTSRTLENNRRNVWFAYEWEENFCKLTISGS 381

QY 464 QSDSRRRRRGVGTSGHLPPEAI---SQYAPQ-----TYDAVWAIALARAEEHWR 515

Db 382 KKEDTDKRCGTG-----QERIGKDSNYEQEGKVQFVIDAVYMAHAL-----HHNKK 427

QY 516 N-----EEQSKLDGFDYTRSDMAWEFLQOMKGLHFLGVSG-PVSFS-GPDRVGTTA 564

Db 428 DLCAADYRGVCPMEQAGG-----KKLLKYRNWNFNFSAGTVPVFNKNGDAPGRYD 478

QY 565 FYQIQ-----RGL----- 572

Db 479 IFQYQTTNTSNPGYRLIQWTDLEQLNIEDMQWKGVREIPASVCTLPCKPQKQKTKG 538

QY 573 -----LEPVALYYPATDALDFRCPRC-----RPVKWHSQ--QVPIAKRVFLKRVATIAPL 620

Db 539 TPCCWTCEPCDGYQYQFD--EMTCQHCPYDQRPNENRTGCDIPLIKLEWHSWPAVIP-- 594

Db 698 LRSQVGVVIAWLGAPP---HSV---IDYEQRTVDPQARGVLCMDSDLSLIGCLG 750

Qy 807 YGGLLVGVVWAEWTRHVKIPALNDSQYIGVSVYV-VITSALVVVLANLI--SERVTL 863

Db 751 YSLLMVTCTVYAKARGVP-EFNEAKPIGFTWYTCIIWLAFVPIFFGTAQSAEKIYI 809

Qy 864 AFTITALLTSTATLCLLFIPLKLDI 891

Db 810 QTTTLTVSLSASVSLGMLYVPTVI 837

RESULT 8

MGR2_HUMAN STANDARD; PRT; 872 AA.

AC Q1416;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE METABOTROPIC GLUTAMATE RECEPTOR 2 PRECURSOR.

GN GRM2 OR GPRC1B OR MGLUR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95346007; PubMed=7620613;

RA Flor P.J., Lindauer K., Puttner I., Ruegg D., Lukic S., Knopfel T.,

RA Kuhn R.;

RT "Molecular cloning, functional expression and pharmacological

RT characterization of the human metabotropic glutamate receptor type

RT 2.;"

RL Eur. J. Neurosci. 7:622-629(1995).

CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS

CC MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.

CC MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN

CC SYNAPTogenesis OR SYNAPTIC STABILIZATION.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE

CC ADULT BRAIN AS WELL AS IN FETAL BRAIN.

CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

CC STRONGEST, TO MGLUR3.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; L35318; AAA76855.1; -

DR GCRDB; GCR.1846; -

DR MIN; 604099; -

DR InterPro; IPR001828; ANF_receptor.

DR InterPro; IPR000337; GPCR_Mgr.

DR Pfam; PF00003; 7tm_3; 1.

DR Pfam; PF01094; ANF_receptor; 1.

DR PRINTS; PR00248; GPCRMRG.

DR PRINTS; PR00593; MTABOTROPICR.

DR PRINTS; PR01052; MTABOTROPICR.

DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS02029; G_PROTEIN_RECEP_F3_4; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;

KW Multigene family.

KW SIGNAL 1 18

FT CHAIN 19 872

FT DOMAIN 19 567

FT TRANSMEM 568 590

FT TRANSMEM 591 604

FT TRANSMEM 605 625

FT II (POTENTIAL).

FT DOMAIN 626 636

FT TRANSMEM 637 655

FT DOMAIN 656 679

FT TRANSMEM 680 700

FT DOMAIN 701 725

FT TRANSMEM 726 747

FT DOMAIN 748 760

FT TRANSMEM 761 783

FT DOMAIN 784 793

FT TRANSMEM 794 819

FT DOMAIN 820 872

FT CARBOHYD 203 203

FT CARBOHYD 286 286

FT CARBOHYD 338 338

FT CARBOHYD 402 402

FT CARBOHYD 547 547

SQ SEQUENCE 872 AA; 95507 MW; 058608C35C701E9D CRC64;

Query Match 5.2%; Score 349.5; DB 1; Length 872;

Best Local Similarity 21.8%; Pred. No. 1.6e-16;

Matches 188; Conservative 114; Mismatches 363; Indels 199; Gaps 31;

Qy 151 GKIVLLGLFELSTSRPRD-----GLSELGAATMAVEHINR-KRLPG----- 193

Db 30 GDVLGLGLFPVHQKGPACDCGVNEHRIQIRLEAMLFALDRINRPHLLPGVRLGAHIL 89

Qy 194 -----YTLVLTNDTCDCGVGDPRFP-----AIYQPTRMVWLGSACSEVTE 239

Db 90 DSCSDTHALFQALDFVRASLSRGADGSHRICPDGSIYATHGDAPTAITVGIGSDVSI 149

Qy 240 SLAKVVPYNNIVQVSGSTSPALSDRRPEPPYFRTYVAPDSSHNPARIAFIRKFGTVT 299

Db 150 QVANLLRLFPQISYASTSAKLSKSDYDFARTVPPDFFOAKAMAEILRFENNTYVST 209

Qy 300 FSONEEVSLAVNNLVTELEAANISCAATI-----TFAATDFKEQL-LLRETDIRIIG 353

Db 210 EASEGDYGETGIEAFEELEARNI-CVATSEKVGRAAFEGVVVRRALLQKPSARVAVL 268

Qy 354 SFQSELAQIICEAYRLRMFGADYAWILHESMA-----NASFTWASDVGWGALESVAGSEGAEGAITIELASYPI 387

Db 269 FTRSEDARELLAASORL---NASFTWASDVGWGALESVAGSEGAEGAITIELASYPI 325

Qy 388 -----PW-----WPDQRTACSNHQLQAVENLIV----- 412

Db 326 DFASVFQSLDPWNNRNPFREFW-EQRFRCFQRDCAAHSLRAVPPPEQSKIMFVNA 384

Qy 413 -----STHNSIVGNVSYGLNNHMFNSQLRKQSAQFHGQDGFSGYGPRIASIA 463

Db 385 VYAMAHAHLNHRALCPNTRLCDAVRPVNGRRLYK---DFVLNVKFDAPFRP---ADT 437

Qy 464 QDSRRRRRGVVGTSGGHLPEALISQAPOTYDAVWATAALRAAEHRRNEEQSKLD 523

Db 438 HNEVRFDR-----FGDGIGRYNIFTY-----LRAGSGRYRQKGYWAE 476

Qy 524 GFDYTRSDMAWEFLQOMKGLHFLGVSGVPVSFG-----PDRVGTAFYQIORGLLEPVA 577

Db 477 GLTLDTSIIPWASPS-----AGPLAASRCSEPCQLONEVKSVPQCEVCWCLICPCQ 526

Qy 578 LYYPATDALDFRCRCRPVKWH-----SGQVPIAKRVFKLRVA-TIAPLAFYTIATLSSVG 632

Db 527 PYEYRLD--EFTCADCGLGYWPNASLTGCFELPQEIYRWGDWAVGPV---TIACLG--- 578

Qy 633 IALAITF-LAENLHFRKLKALKSPKLSNITAVCIFYATVILLGLDHSILPSAEDSF 691

Db 579 -ALATFLVLGVFVRHNATPVVKASGRELCYLLGGVFLCYCMTFTFIKAPST----- 629

Qy 692 ATVCTARVYLLSAGFSLAFSGMFAKTYRVHRIF--TRTGSVFKDKMLQDIQILLVGLL 749

Db 630 -AVCTLRRLGLGTAFSVCYSAALLTKNRIARIFGGARGAQ-RPRFISPASVAICLALI 687

Qy 750 LVDALLTVLVVYVTDPMERHLNHLNLTLEISATDRSVV-YQPQVEVCRSOHTQWLSVLYAYK 808

```

Db 707 LQVVGMLAWLCARPP-----HSV---IDYEQRTVDPEARGVLKCDMSDLSLIGLGYSL 759
QY 810 LLLVGVYMAWETRHVKIPALNDQSYGVSV--VITSIVVVLANLI--SERVTLAPI 866
Db 760 LLMVTCFVYAIKARGVP-ETNEAKPIGFTMTTCIIWLAFVPIFFGTAQSAEKIYIQT 818
QY 867 TITAILTSTATLCLFIPKLHDI 891
Db 819 TLVSVLSASVSLGMLYVPKTYVI 843

RESULT 7
MGR6_RAT
ID MGR6_RAT STANDARD; PRT; 871 AA.
AC P35349;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 6 PRECURSOR.
GN GRM6 OR GPRC1F OR MGLUR6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Retina;
RX MEDLINE=93280152; PubMed=8389366;
RA Nakajima Y., Iwakabe H., Akazawa C., Nawa H., Shigemoto R.,
RA Nakanishi S.;
RT "Molecular characterization of a novel retinal metabotropic glutamate
RT receptor mGluR6 with a high agonist selectivity for L-2-amino-4-
RT phosphonobutyrate."
RL J. Biol. Chem. 268:11868-11873(1993).
CC -1- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: RESTRICTEDLY EXPRESSED IN THE INNER NUCLEAR
CC LAYER OF THE RETINA.
CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D13963; BAA03066.1;
CC PIR: A46742; A46742.
CC GCRdb: GCR_0623;
CC InterPro: IPR001828; ANF_receptor.
CC InterPro: IPR000337; GPCR_Mgr.
CC Pfam: PF00003; 7tm.3; 1.
CC Pfam: PF01094; ANF_receptor; 1.
CC PRINTS: PR00248; GPCR_MGR.
CC PRINTS: PR00593;
CC PRINTS: PR01056; MTABOTROPICR.
CC PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE: PS00259; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family; Vision.
CC -----
KW SIGNAL 1 18
KW CHAIN 19 871
KW DOMAIN 19 579
KW TRANSMEM 580 602
KW DOMAIN 603 616
KW METABOTROPIC GLUTAMATE RECEPTOR 6.
KW EXTRACELLULAR (POTENTIAL).
KW I (POTENTIAL).
KW CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 617 637
FT DOMAIN 638 648
FT TRANSMEM 649 667
FT DOMAIN 668 691
FT TRANSMEM 692 712
FT DOMAIN 713 742
FT TRANSMEM 743 764
FT DOMAIN 765 777
FT TRANSMEM 778 800
FT DOMAIN 801 813
FT TRANSMEM 814 839
FT DOMAIN 840 871
FT CARBOHYD 290 290
FT CARBOHYD 445 445
FT CARBOHYD 473 473
FT CARBOHYD 561 561
SQ SEQUENCE 871 AA; 95089 MW; 9F70B4D6A13B186D CRC64;

Query Match 5.5%; Score 367; DB 1; Length 871;
Best Local Similarity 21.8%; Pred. No. 9.1e-18;
Matches 189; Conservative 130; Mismatches 361; Indels 188; Gaps 32;

QY 151 GKIVLLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLLPG----- 193
DB 31 GGLTGLGLFPVH-ARGAAGRACGKKEQGVHRLEAMLYALDRVNDADPELLPGVRLGARL 89
QY 194 -----YTLELVNDTQ-----CDPGGVDRFFHAYITOPSTRMVMLL 230
DB 90 LDTCSRDTYALEQALSFVQALIRGGDGEASVRCPGV-----PPIRSAPPERVAVV 143
QY 231 GSACSEVTESLAKVVPYNNIVQVSGTSPALSDRRPEFYFRTVAPDSSHNPIARIFIR 290
DB 144 GASASSVSIINVANVLRIFAIPQISYASTAPELSDTYDFSRVVPDYSQAQAMVDIVR 203
QY 291 KFGWGTVTTSQNEVHSLAVNNLV-TELEAANISCAATITFAAT-----DFKEQLLLIRE 345
DB 204 ALGWNVYSTLASEGNYGESGVEAFVQISREAGGVCIAGSIKIPREPKEGFHKVIRRLME 263
QY 346 TDRIRIIGSFQSOELAPOLCEAYRLRMFGADYAWILHESMGAPWMPDQRTACSNHELQLA 405
DB 264 TPNARGIIIFANEDDIRRVLEATQANLTGHFLVGSWSGKISIP-----ILNLE 314
QY 406 VENLIVVSTHNSIVGNVSVSGLNNHMFNSQLRKQSAQFHQDGGFGSGYGRISATAQTS 465
DB 315 EAVGAI-----TILPKRASIDGPDQYFMYSTRSLENNRRNIWEAFWEENFNCKLTSSGQS 370
QY 466 DSRRRRRGVVGTSGHGLFPPEAISQ---YAPQ-----TYDAWATAIALRAAE----- 511
DB 371 DDSTRKCTG-----BERIQDSAYEQEGKVQFVIDAVYATAHALHSMHQALCPGH 420
QY 512 -----HWRR-----NEEQSKLDGFDY----- 527
DB 421 TGLCPAMEPTDGRITLLHYIRAVRNGSAGTVPVFNENGDAPGRYDIFQYQATNGSASGG 480
QY 528 -----TRSDMAWEFLQOMKGLHFLGVSGVPVSFSGPDRVGTTAFYQIQIGLLEPVA 577
DB 481 YQAVGQWAEALRLDM--EVLRWSDGPHV---PPSQCSLP--CGPGERKKVKGV--PCC 531
QY 578 LYPATDAL-----DFRCPRC-----RPVKHSGGVPIAKRVFKLRVATIAPIAFYTIATL 628
DB 532 WHCEACDGYRFQVDEFTCEACPGDMRPTPNHTGCRPT-----VRLTWSSPWAALPL-LL 586
QY 629 SSVGIALAIATFLAPNLHFRKKAIKLSPKLSNITAVCCIFVYATVILLGLDHSHTLPRAE 688
DB 587 AVLIGMATTTIMATFMRHNDTPIVRASGRELSVLLTGIFLIYATITFLM-----VA 637
QY 689 DSFATVCTARVYLLSAGFSIAFGSMFAKTYRVHRTFTT-TGSVFKDKMLQDIQLILLVGG 747
DB 638 EPCAICAARLLGLLGLTLLSISALLTKNRIYRIFEOGKRKSVTPPPPISTPSQLVITFG 697
QY 748 LLLVDALLVTVWVYDPMERHNLTLLEISATDRSVVYQPOVE-VCRSQHTQTWLSVLVA 806

```

[illegible]

CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC -!- CAUTION: ISOFORM 1E HAS BEEN CALLED 1C IN REF.3.
 CC -----
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 CC -----
 CC EMBL; Y10369; CAA71398.1; -
 CC EMBL; Y10370; CAA71399.1; -
 CC EMBL; AB016160; BAA34708.1; -
 CC EMBL; AB016161; BAA34709.1; -
 CC EMBL; AF110797; AAD19656.1; -
 CC EMBL; AF110797; AAD19656.1; JOINED.
 CC EMBL; AF110797; AAD19657.1; -
 CC EMBL; AF110797; AAD19657.1; JOINED.
 CC EMBL; AF110797; AAD19658.1; -
 CC EMBL; AF110797; AAD19658.1; JOINED.
 CC EMBL; AF110797; AAD19659.1; -
 CC EMBL; AF110797; AAD19659.1; JOINED.
 CC HSP; P10998; 1YVC.
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC InterPro; IPR000436; Sushi_SCR_CCP.
 CC Pfam; PF00003; 7tm3_1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC Pfam; PF00084; sushi; 2.
 CC PRINTS; PR01176; GABARECEPTR.
 CC PRINTS; PR01177; GABARECEPTR.
 CC SMART; SM00032; CCP; 2.
 CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
 CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 CC SIGNAL 1 16
 CC CHAIN 17 991
 CC
 CC DOMAIN 17 590
 CC TRANSMEM 591 611
 CC DOMAIN 612 630
 CC TRANSMEM 631 651
 CC DOMAIN 652 666
 CC TRANSMEM 667 687
 CC DOMAIN 688 709
 CC TRANSMEM 710 730
 CC DOMAIN 731 797
 CC TRANSMEM 798 818
 CC DOMAIN 819 834
 CC TRANSMEM 835 855
 CC DOMAIN 856 863
 CC TRANSMEM 864 884
 CC REPEAT 29 95
 CC REPEAT 99 156
 CC DOMAIN 885 991
 CC DOMAIN 901 955
 CC TRANSMEM 901 955
 CC CARBOHYD 23 23
 CC CARBOHYD 83 83
 CC CARBOHYD 408 408
 CC CARBOHYD 439 439

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 501 501 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 513 513 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 163 MLLLLVPLFLRPLGAGQTPNATSECOIHPWEGGIR
 FT YRGLTRQVKAINFLPVGYELEYVCRGEEVGVKVKCLA
 FT NGSWTDMTPSRVCYRICKSVLTLENGKVFLLTGGDLPALDG
 FT ARVEFCDPFLHVSRSVCQSGQWSTPKPHQCQVNRTPH
 FT -> MGPGCPTPVGMPLPLLLVMAAGVAPVWASHPSHLPRP
 FT HPRVPHPS (IN ISOFORM 1B, ISOFORM 1C AND
 FT ISOFORM 1D).
 FT MISSING (IN ISOFORM 1A, ISOFORM 1B AND
 FT ISOFORM 1D).
 FT VARSPLIC 771 801 KEERVELHQQLRQQLRRRHPTTPDPDGGGLPRGSEP
 FT VARSPLIC 935 991 PDLRSCDGRVHLLYK -> VCGDKQPGPPVSEGLPVVGP
 FT SIEV (IN ISOFORM 1D).
 FT MUTAGEN 247 247 S->A: NO CHANGE IN THE AFFINITY FOR GABA.
 FT MUTAGEN 268 268 S->A: NO CHANGE IN THE AFFINITY FOR GABA.
 FT MUTAGEN 269 269 S->A: DECREASE IN THE AFFINITY FOR GABA.
 FT SEQUENCE 991 AA; 111533 MW; 012CD293D4B44A2 CRC64;
 Query Match 14.5%; Score 971; DB 1; Length 991;
 Best Local Similarity 28.7%; Pred. No. 3.6e-60;
 Matches 259; Conservative 157; Mismatches 364; Indels 124; Gaps 18;
 QY 96 RROQLNLSHNLPGSTNASHAHLLNLPQRQYIKVQNVFESERRMSPAEMQNHGKIVL 155
 DB 125 RVEFRCDPDLHLVSSRSVCQSGQWSTP-KPHCQVNRTPHSERR-----AVYI 171
 QY 156 LGLFELSTSRGPRPDGLSELGAATMAVHINRKR-LLPGYILELVNTDQCDPGVGVDRF 214
 DB 172 GALPMS---GGWPGGQACQAVEMALADVNSRRDILPDYELKLHHDSCDPPGQATKYL 228
 QY 215 FHAIYTOPSTRMVMVLGSGACSEVTESLAKVPYVNIQVSEGSTSPALSDREFFYFRT 274
 DB 229 YELLYNDP---IKIILMPGSSVTLVAEAAARMNLLVLSYSSSPALSNRQFFTFRT 285
 QY 275 VAPDSSHNPARIATFRKFGWGTVTTFSQNEEVHSLAVNVLTELEAANISCAATITFAAT 334
 DB 286 HPSATLHNPTRVKLFKWKWKKIATIQTTVEFTSLDLEERVKEAGIE---ITFRQS 341
 QY 335 DFKEQLL---LLRETDFRIIGSFQSQELAPQILCAYRLRMFGADYAWILHESGAPWMP 391
 DB 342 FFSDPAVPVKNLKQDARIIVGLFEYETEARKVFCVYKERLFGKYYVFLIGWADNWFK 401
 QY 392 --DORTACSNHELOAVENLVVSTHNSIVGNVSYSGLNHMFNSOLRKQSAQFHGDG 449
 DB 402 TYDPSINCTVEEMTEAVEGHITTEIVMLNPANTRTSISNMTSQEFVEKLTK----- 451
 QY 450 FGSGYGPRIATAATQSDSRRRRRGVVGTSQGHLPPEAISOVAPQTYDAVWAIALRAA 509
 DB 452 -----RLKRHPETGG-----FQEAPLAYDAIWAIALALNKT 483
 QY 510 EHWRRNEOSKLDGFDYTRSDMAWEFLQMGKHLFGLVSGPVSF-SGPDRTVGTTFATYQI 568
 DB 484 SGGGGRS--GVRLEDFNNTQITDIYRAMSSSFEVSGHGVFVDFASGRSMAWTLIEQL 541
 QY 569 ORGELLEVALYYPATDALDFRCPRCPVKHSGQVPIAKRVKFLRVATIAPLAFYTIATL 628
 DB 542 QGSYKKIGYDSTKDDLSW----SKTDKWIIGGSPADQTLVIKTRFLSQKLFISVSVL 597
 QY 629 SSVGIALAITPLAFNLHPRKLIKATKLSPPKLSNITFVAGCIFVYATVILLGLDHSHP 688
 DB 598 SSLGIVLAVCLSNFYNSHVRYIQNSQPNLNNLTAVGCSLALAAVFLGLDGYHI--GR 655
 QY 689 DSFATVCTARVYLLSAGFSLAFSGMFAKTYRVHRITRTGVSFKD-----KMLQDIQLI 742
 DB 656 SQPFVVCQARLWLLGLGFSIGYSNFTKIWWVHTVETK-----KEEKKEWRKTL 710
 QY 743 LLVGGLLLVALLVTLVWVTPDPMERHLNLTLSATRSRVVYQVQVCRSQHTQTLW- 801
 DB 711 ATVGLLVGMVLTALAIQIVDPLHRTIETFAKEPKEDIDVLSILQLEHCSKSKMNTWLG 770

QY 454 YGPRISATQSDRRRRRGGVGTSGHLPPEAISQAPOTYDAVNAIALRAAEHWH 513
Db 452 -----RLKRHPETGG-----FOEAPLAYDAINALALANKTSGG 487
QY 514 RRNEEQSKLDFDYTRSDMAWEFLQMGKHLFLGVSGVSPF-SCPDRTGVTAFYQIORGL 572
Db 488 GRS--GVRLEDFNNQTIITDQYRAMNSSFEQVSGHVDFDASGRMAWFLIEOLOGGS 545
QY 573 LEFVALYYPATDALDFRCRPRVKWHSQGVPIAKRVFKLRVATIAPIAFYTIATLSVG 632
Db 546 YKIGIYDSTKDDLSM---SKTDKWLIGSGPPADQTLVIKTRFELSKQLFISVSLSLG 601
QY 633 IALATFLAENLHFRKLKATKSPKUSNTAVGCFIVYATVILLGLDHDHSLPLSAEDSFA 692
Db 602 IVLAVCLSENIYNSHRYIQNSQPNLNLTAAGCSLALAAVFLPLGLDGYHI--GRSOPF 659
QY 693 TVCTARVYLLSAGFSLAFSGMEAKTYRVHRTFTGVSFXD-----KMLQDIQILLLVG 746
Db 660 FVCOARLWLLGLFSLGYSMTFKIMWHTVTK-----KEEKKEWRTLEPWKLKLYATVG 714
QY 747 GLLVDALLVTLWVVDPMERHLNLTLEISATDRSVYVQVGVCRSQHTQTLWSLVLYA 806
Db 715 LVGMDLITLAINQIYDPLHRTTETFAKEPKEDIDVSLIPOLHCSKKNWTLGIFYG 774
QY 807 YGGLLVGVYMAWETHRVKIPALNDSQYIGSVSYSVITSATVIVVLANLISERTVLAFI 866
Db 775 YGGLLLGLIFLAYETKSVSTEKINDHRAVGMATYNAVLCILITAPVTMILSSQDDAFA 834
QY 867 TITALLITSTATLCLLFIPLKHDHWARDIIDPVHSMGLKMECNTRFVDDRELOY 926
Db 835 FASLAVFSSYITLVFLVFPKMRILTRGEMQSEAPQTMKTGSSTN-----NNEEKSR 888
QY 927 RVEQNVRYKKEIQALDAERKLERLES 955
Db 889 LLEKENRELEKIATKEERVSERLHQLOS 917
RESULT 5
ID GBRL_RAT STANDARD: PRT: 991 AA.
AC Q92004; O08620; O08621; Q920F9; Q92308;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GB1).
GN GABBR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC STRAIN-RICO; TISSUE=brain cortex, and Cerebellum;
RX MEDLINE=9722131; PubMed=9069281;
RA Kaupmann K., Huggel K., Heid J., Flor P.J., Bischoff S., Mickel S.J.,
RA McMaster K., Angst C., Bittiger H., Froestl W., Bettler B.,
RT "Expression cloning of GABA(B) receptors uncovers similarity to
RT metabotropic glutamate receptors.";
RL Nature 386:239-246(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
RC TISSUE=Cerebellum;
RX MEDLINE=99092370; PubMed=9875211;
RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
RA Iano K., Taniyama K.,
RT "Cloning and tissue distribution of novel splice variants of the rat
RT GABAB receptor.";
RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1E).
RC STRAIN-Wistar; TISSUE=Hippocampus;

RX MEDLINE=9938283; PubMed=10457184;
RA Pfaff T., Malitschek B., Kaupmann K., Prezeau L., Pin J.-P.,
RA Bettler B., Karschke A.,
RT "Alternative splicing generates a novel isoform of the rat
RT metabotropic GABA(B)R1 receptor.";
RL Eur. J. Neurosci. 11:2874-2882(1999).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.
RC TISSUE=Brain;
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chatauneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
RT functional GABAB receptor activity.";
RL J. Biol. Chem. 274:7607-7610(1999).
RN [5]
RP TISSUE DISTRIBUTION.
RC TISSUE=Brain;
RX MEDLINE=20121644; PubMed=10658574;
RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
RA Ng G.Y.K.;
RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
RT forms.";
RL Bioorg. Med. Chem. 7:2697-2704(1999).
RN [6]
RP R1A-R2 INTERACTION.
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of Heteromer Formation in GABA-B Receptor Function.";
RL Science 283:74-77(1999).
RN [7]
RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
RX MEDLINE=20159055; PubMed=10692480;
RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
RA Kaupmann K., Pin J.-P.;
RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)
RT binding at GABA(B) receptors: involvement of serine 269 of the
RT GABA(B)R1 subunit.";
RL Mol. Pharmacol. 57:419-426(2000).
CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC STIMULATED BY G-PROTEINS THAT INHIBITS ADENYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -1- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A, 1B, 1C, 1D AND 1E (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL
CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS

CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION.
 CC -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA (BY
 CC SIMILARITY).
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MOROVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1A (SHOWN HERE), 1B, 1C AND 1D;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC
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 CC
 CC EMBL; AF114168; AAD22194.2; -
 CC EMBL; AL078630; CAB44980.1; -
 CC EMBL; AL078630; CAB44991.1; -
 CC EMBL; AL078630; CAB44992.1; -
 CC EMBL; AL078630; CAB44993.1; -
 CC EMBL; AF120255; AAG29341.1; -
 CC EMBL; AF008649; AAG29338.1; -
 CC MGD; MGI:1860139; Gabbr1.
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC InterPro; IPR000436; Sush1_SCR_CCP.
 CC Pfam; PF01094; ANF_receptor; 2.
 CC Pfam; PF00003; 7tm_3; 1.
 CC Pfam; PF00084; sush1; 2.
 CC PRINTS; PR01176; GABABRECEPTR.
 CC PRINTS; PR01177; GABABIRECEPTR.
 CC SMART; SM00032; CCP; 2.
 CC PROSITE; PS00979; G.PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC PROSITE; PS00980; G.PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC PROSITE; PS00981; G.PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC PROSITE; PS00981; G.PROTEIN_RECEP_F3_4; 1.
 CC PROSITE; PS02059; G.PROTEIN_RECEP_F3_4; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Coiled coil; Repeat; Alternative splicing.
 CC SIGNAL 1 16
 CC CHAIN 17 960
 CC
 CC SUBUNIT 1.
 CC DOMAIN 17 590
 CC TRANSMEM 591 611
 CC DOMAIN 612 630
 CC TRANSMEM 631 651
 CC DOMAIN 652 666
 CC TRANSMEM 667 687
 CC DOMAIN 688 709
 CC
 CC EXTRACELLULAR (POTENTIAL).
 CC I (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).
 CC II (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC III (POTENTIAL).
 CC CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 710 730
 FT DOMAIN 731 767
 FT TRANSMEM 768 788
 FT DOMAIN 789 803
 FT TRANSMEM 804 824
 FT DOMAIN 825 832
 FT TRANSMEM 833 853
 FT DOMAIN 854 960
 FT REPEAT 99 95
 FT REPEAT 29 156
 FT DOMAIN 868 924
 FT CARBOHYD 23 23
 FT CARBOHYD 83 83
 FT CARBOHYD 408 408
 FT CARBOHYD 439 439
 FT CARBOHYD 481 481
 FT CARBOHYD 501 501
 FT CARBOHYD 513 513
 FT VARSPLIC 1 163
 FT
 FT TRANSMEM 771 960
 FT DOMAIN 904 960
 FT VARSPLIC 904 960
 FT
 FT CONFLICT 7 8
 FT CONFLICT 46 46
 FT CONFLICT 618 618
 FT CONFLICT 642 642
 FT CONFLICT 721 721
 FT CONFLICT 812 812
 FT CONFLICT 869 869
 FT CONFLICT 921 921
 FT SEQUENCE 960 AA; 108216 MW; E4B5A9401E23E8B4 CRC64;
 SQ
 Query Match 14.88; Score 990.5; DB 1; Length 960;
 Best Local Similarity 29.6%; Pred. No. 1.4e-61;
 Matches 257; Conservative 156; Mismatches 363; Indels 93; Gaps 17;
 QY 100 RLNSHNLPGSTNASHAHLLNLPQRQYKLVNOVFESERRMSPAEMQRNHGKTVLGLGF 159
 DB 129 RCDPDFHLVGSRRSICSGQWSTP--KPHCQVNRTPISERR-----AVIGALF 175
 QY 160 ELSTSRGPRPDGLSELGAATMAVEHINRKR--LLFCYTLLELVNTDQCDDPGVDRFFHAI 218
 DB 176 PMS---GGWPGGQACQPAVENALEDVNSRRDILPDYELKLHSDKCDPGQATLYELL 232
 QY 219 YTOPSTWMLLGSACSEVETSLAKVPYWNIVQVSGSTSPALSDREFFYFTVAPD 278
 DB 233 YNDP---IKIILMPGCSVSTLVAEAAARNWNLIVLSYSSSPALSNRQRFPTFTTHPSA 289
 QY 279 SSNPARIATIRKFGMGTVTTFSSQNEEVHSLAVNNLVTELEAANISCAATITFAATDPKE 338
 DB 290 TLHNPTRVKUFERKWKKIATIQOTTEVFTSTLDDLEERVKEAGIE----ITFRQSFSD 345
 QY 339 QLL---LLRETDTRIIGSFISOELAPQLCEAYRLRRMGADYAWILHESMGAPWMP--DQ 393
 DB 346 PAVPVKNLRODARIIVGLVETETARKVFCVYKERLFGKKYVWFLIGWADNFKYIDP 405
 QY 394 RTACSNHELQLAVENTLIWVSTHNSIVGNVNSYSLNNHMFNSQLRKQSAOPHGQDGFSG 453
 DB 406 SINCTVEEMTEAVEGHITTEIVMLNPANTRISINMTSQEFVEKLTK----- 451

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DR EMBL; AJ225028; CAA12359.1; -
DR EMBL; AJ225029; CAA12360.1; -
DR EMBL; AJ012185; CAA09939.1; -
DR EMBL; AJ012186; CAA09940.1; -
DR EMBL; AF099148; AAC98508.1; -
DR EMBL; Y11044; -; NOT_ANNOTATED_CDS.
DR EMBL; AJ012187; CAA09941.1; -
DR EMBL; AJ010170; CAA09031.1; -
DR EMBL; AJ010171; CAA09031.1; JOINED.
DR EMBL; AJ010172; CAA09031.1; JOINED.
DR EMBL; AJ010173; CAA09031.1; JOINED.
DR EMBL; AJ010174; CAA09031.1; JOINED.
DR EMBL; AJ010175; CAA09031.1; JOINED.
DR EMBL; AJ010176; CAA09031.1; JOINED.
DR EMBL; AJ010177; CAA09031.1; JOINED.
DR EMBL; AJ010178; CAA09031.1; JOINED.
DR EMBL; AJ010179; CAA09031.1; JOINED.
DR EMBL; AJ010180; CAA09031.1; JOINED.
DR EMBL; AJ010181; CAA09031.1; JOINED.
DR EMBL; AJ010182; CAA09031.1; JOINED.
DR EMBL; AJ010183; CAA09031.1; JOINED.
DR EMBL; AJ010184; CAA09031.1; JOINED.
DR EMBL; AJ010185; CAA09031.1; JOINED.
DR EMBL; AJ010186; CAA09031.1; JOINED.
DR EMBL; AJ010187; CAA09031.1; JOINED.
DR EMBL; AJ010188; CAA09031.1; JOINED.

Query Match      14.8%; Score 991.5; DB 1; Length 961;
Best Local Similarity 29.6%; Pred. No. 1.2e-61;
Matches 257; Conservative 157; Mismatches 362; Indels 93; Gaps 17;

QY 100 RLNSHNLPSTNASHAHLLNLPORYLKVNQVFSERMSPAEMORNGKILVLLGLF 159
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 RCDPDLHLVGSRSICSGQWSTP--KPHCOVNRTPHSERR-----AVYIGALF 176

QY 160 ELSTSGPRPDGLSELGAATMAVEHINRKR-LIPGYILELVNTQCDPGVGVDRFHA 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 PMS---GGWPGGACQAPVEMALDVSRRDILPDYELKLIHHDKCDPGQATKLYELL 233

QY 219 YTOPSTRMVLGSGACSEVESLAKVVPYVNIQVSGSTSPALSDRRRPFYFRTVAPD 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 YNDP---IKIILMPGCSVSTLVAERAMWNLIIVLSTGSSSPALSNRQRPFTFTRHPSA 290

QY 279 SSHNPARIAFIRKFGTGTFTFSQNEEVHSLAVNNLVTELEAANISCAATITFAATDFKE 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 TLHNPTRVKLFKXGKKIATIQOTTEVFTSLDLDLEVRKEAGIE---ITFRQSFSD 346

QY 339 QLL---LLRETDRRIIGSFQELAPQILCEAVRLRMFGADYAWILHESGAPWMP--DQ 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 PAVPVNKLKQDRAIVGLFYETEARVFCVEYKERLFGKYVWFLIGWADNWFKIYDP 406

QY 394 RTACSNHELQLAVENTLVVSTHNSIVGNVYSYSLNNHMFNSOLRKOSAFHGDGFGSG 453
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 407 SINCTVDEMTAEVGHITTEIVMLNPANTNISNMTSQEFVEKLTK-----452

QY 454 YGPRISIAATQSDRRRRRRGVGTSGHLFPFAISQYAPQTDVAVMAIALRAAEHW 513
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 453 -----RLKRHPETGG-----FQEAFLAYDAIWAIALANKTSGGG 488

QY 514 RNEEOSKLDGFDYTRSDMAWEFLQMGKLUHFLGVSGPVSF-SGPDRGVGTATFYQIQGL 572
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 489 GRS--CVRLEDENYNNQITDQIYRAMNSSFEVGHVVFSDASGRMAWTLIEQLQGS 546

QY 573 LEPVALYYPATDALDFRCRCRPVKHSGOVPIAKRVFKLRVATIAPIAFYTTATLSVG 632
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 547 YKKIGYDSTKODLSW-----SKTDKIGGSGPPADQTLVIKTRFLSKQLFISVSLSLG 602
```

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QY 633 TALAITFLAFNLHFRKLKALKLSSPKLSNITAVGCFIVYATVILLGLDHTSLPSAEDSFA 692
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 IIVAVVCLSNFYINSHYIQNSQPNLNNLTAVGCSLAAAVFPLGLDGYHI--GRNQPP 660
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 693 TVCTARVYLLSAGSLAFSGSMFAKTVRVHRIERTGTSVKFD-----KMLQDIQIILLVG 746
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 661 FVCQARLLWLLGLGSLGSGSMFTKIWWHTVFTK-----KEEKKWRKTLFEPKLYATVG 715
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 747 GLLVDALLVTLWVYVTPMERHLNLTLEISATDRSVVYQPOVEVCRSQHTQTLWSLYA 806
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 716 LLVGMVLTALAIQIIVDPLHRTIETFAKEPKEDIDVSLPQLEHCSRRKMTWLGIFVG 775
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 807 YKGLLVGVVYNAWETRVHKVIPALNDSQVIGSVYSVITSIAVVVLANLISERVTLAPI 866
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 776 YKGLLLGLIFLAYETKSVSTEKINHRAVGMAYINAVLCLTIPVMTILSSQDDAFA 835
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 867 TITAILTSTTATCLLFIPLKLDIWARNDIIDPVHSMGLKMECNTRFVVDRELO 926
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 836 FASLAIVFSSYITLVLPVKMRRLITRGWQSEADQTMKTGSTN-----NNEEKSR 889
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 927 RVEONRVYKREIQALDAEIRKLERLES 955
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 890 LLEKENRELEKIIAEKEERVSSELRLQLOS 918
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
GBR1_MOUSE STANDARD; PRT: 960 AA.
AC Q9WV18; Q9WV15; Q9WV16; Q9WV17; Q9WU48;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
GN GABBR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RA "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RL receptor.";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
[2]
SEQUENCE FROM N.A. (ISOFORM 1B).
RA Younger R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (ISOFORM 1B).
RA Lamp K., Humeny A., Nikolic Z., Becker C.-M.;
RA "Cloning of the murine GABABR1b receptor.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A. (ISOFORM 1A).
RA Humeny A., Lamp K., Nikolic Z., Becker C.-M.;
RA "Mouse GABA-B receptor cDNA sequence.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[5]
RIA-R2 INTERACTION.
RX MEDLINE=99102694; PubMed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of heteromer formation in GABAB receptor function.";
RL Science 283:74-77(1999).
CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.
```

RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99087321; PubMed=9872316;
 RA White J.H., Wise A., Main M.J., Green A., Fraser A., Disney G.H.,
 RA Barnes A.A., Enson P., Foord S.M., Marshall F.H.;
 RT "Heterodimerization is required for the formation of a functional
 RT GABA(B) receptor.";
 RL Nature 396:679-682(1998).
 [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP TISSUE=Brain;
 RC Stropp U., Raming K.;
 RA "Human mRNA for GABA-B1a receptor.";
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP TISSUE=Fetal brain;
 RC MEDLINE=98440782; PubMed=9753614;
 RX Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,
 RA Zelante L., Gasparini P.;
 RT "GABA (gamma-amino-butyric acid) neurotransmission: identification and
 RT fine mapping of the human GABAB receptor gene.";
 RL Biochem. Biophys. Res. Commun. 250:240-245(1998).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RP MEDLINE=99014802; PubMed=9798068;
 RA Goel V.L., Choi J., Ahn J., Bowlus C.L., Raha-Chowdhury R.,
 RA Gruen J.R.;
 RT "Human gamma-aminobutyric acid B receptor gene: complementary DNA
 RT cloning, expression, chromosomal location, and genomic organization.";
 RL Biol. Psychiatry 44:659-666(1998).
 [6]
 RN SEQUENCE FROM N.A. (ISOFORM 1C).
 RP TISSUE=Cerebellum;
 RC Fraser N.J.;
 RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
 RP TISSUE=Fetal brain;
 RC MEDLINE=20184290; PubMed=9933300;
 RX Peters H.C., Kaemmer G., Volz O.;
 RA Epplen J.T., Sander T., Riess O.;
 RT "Mapping, genomic structure, and polymorphisms of the human GABAB1
 RT receptor gene: evaluation of its involvement in idiopathic
 RT generalized epilepsy.";
 RL Neurogenetics 2:47-54(1998).
 [8]
 RN SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RP Younger R.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 [9]
 RN SEQUENCE FROM N.A. (ISOFORM 1A).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99108069; PubMed=9889352;
 RA Makoff A.;
 RT "Molecular cloning of human GABAB1 and its tissue distribution.";
 RL Brain Res. Mol. Brain Res. 64:137-140(1999).
 [10]
 RN SEQUENCE FROM N.A. (ISOFORM 1B).
 RC TISSUE=Prostate;
 RX MEDLINE=20493604; PubMed=10906333;
 RA Schwarz D.A., Barry G., Eliasof S.D., Petroski R.E., Conlon P.J.,
 RA Maki R.A.;
 RT "Characterization of gamma-aminobutyric acid receptor GABAB(1e), a
 RT GABAB(1) splice variant encoding a truncated receptor.";
 RL J. Biol. Chem. 275:32174-32181(2000).
 [11]
 RN VARIANTS VAL-20 AND SER-489.
 RX MEDLINE=99332163; PubMed=10402495;
 RA Sander T., Peters C., Kaemmer G., Samochowicz J., Zirra M.,
 RA Mischke D., Ziegler A., Kaupmann K., Bettler B., Epplen J.T.,
 RA Riess O.;
 RT "Association analysis of exonic variants of the gene encoding the

RT GABAB receptor and idiopathic generalized epilepsy.";
 RL Am. J. Med. Genet. 88:305-310(1999).
 [12]
 RN R1A-R2 INTERACTION.
 RP MEDLINE=20237752; PubMed=10773016;
 RX Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr.,
 RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
 RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
 RT receptors with truncated receptors and metabotropic glutamate
 RT receptor 4 supports the GABA(B) heterodimer as the functional
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 RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
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 RN R1A-R2 INTERACTION.
 RP MEDLINE=99102694; PubMed=9872744;
 RX Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of heteromer formation in GABAB receptor function.";
 RL Science 283:74-77(1999).
 CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCICEPTION. ACTIVATED BY (-)-BACLOFEN, CGP27492 AND BLOCKED
 CC BY PHACLOFEN.
 CC -!- FUNCTION: ISOFORM 1E FUNCTION MAY BE TO REGULATE THE AVAILABILITY
 CC OF FUNCTIONAL GABA-B-R1A/GABA-B-R2 HETERODIMERS BY COMPETING FOR
 CC GABA-B-R2 DIMERIZATION. THIS COULD EXPLAIN THE OBSERVATION THAT
 CC CERTAIN SMALL MOLECULE LIGANDS EXHIBIT DIFFERENTIAL AFFINITY FOR
 CC CENTRAL VERSUS PERIPHERAL SITES.
 CC -!- COPACITOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN. ISOFORM 1E (WITHOUT C-TERMINAL INTRACELLULAR DOMAIN) IS
 CC UNABLE TO DIMERIZE VIA A COILED-COIL INTERACTION WITH GABA-B-R2.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE. ISOFORM 1E CAN ALSO BE SECRETED.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1A (SHOWN HERE), 1B, 1C, 1D AND
 CC 1E/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORMS
 CC CORRESPONDING TO THE FULL RECEPTOR ARE ESSENTIALLY FOUND IN THE
 CC CENTRAL NERVOUS SYSTEM (CNS). ISOFORM 1E IS THE MAJOR ISOFORM IN
 CC ALMOST ALL PERIPHERAL TISSUES. IT MAY ACT AS AN ANTAGONIST OF
 CC GABA-B RECEPTORS, BEING ABLE TO DISRUPT THE NORMAL ASSOCIATION
 CC BETWEEN ISOFORM 1A AND GABA-B-R2.
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN AND WEAKLY IN HEART,
 CC SMALL INTESTINE AND UTERUS. MOSTLY EXPRESSED IN GRANULAR CELL AND
 CC MOLECULAR LAYER FOR ISOFORM 1A AND IN PURKINJE CELLS FORM ISOFORM
 CC 1B. ISOFORM 1E IS PREDOMINANTLY EXPRESSED IN PERIPHERAL TISSUES AS
 CC KIDNEY, LUNG, TRACHEA, COLON, SMALL INTESTINE, STOMACH, BONE
 CC MARROW, THYMUS AND MAMMARY GLAND.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE
 CC LINKER REGION BETWEEN THE TRANSMEMBRANE DOMAIN 3 (TM 3) AND THE
 CC TRANSMEMBRANE DOMAIN 4 (TM 4) PROBABLY PLAY A ROLE IN THE
 CC SPECIFICITY FOR G-PROTEIN COUPLING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PRO0248; GPCRMR.
DR PRINTS: PRO1176; GABAB2RECEPTR.
DR PRINTS: PRO1177; GABAB1RECEPTR.
DR PRINTS: PRO1178; GABAB2RECEPTR.
DR PROSITE: PS00099; PRO_RICH; 1.
DR PROSITE: PS00979; G_PROTEIN_RECEP_F3_1; FALSE_NEG.
DR PROSITE: PS00980; G_PROTEIN_RECEP_F3_2; FALSE_NEG.
DR PROSITE: PS00981; G_PROTEIN_RECEP_F3_3; FALSE_NEG.
DR PROSITE: PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Postsynaptic membrane; Coiled coil; Alternative splicing;
KW Polymorphism.
FT SIGNAL 1 41
FT CHAIN 42 941
FT DOMAIN 42 483
FT TRANSMEM 484 504
FT DOMAIN 505 522
FT TRANSMEM 523 543
FT DOMAIN 544 551
FT TRANSMEM 552 572
FT DOMAIN 573 597
FT TRANSMEM 598 618
FT DOMAIN 619 654
FT TRANSMEM 655 675
FT DOMAIN 676 691
FT TRANSMEM 692 712
FT DOMAIN 713 720
FT TRANSMEM 721 741
FT DOMAIN 742 941
FT CARBOHYD 781 819
FT CARBOHYD 90 90
FT CARBOHYD 288 298
FT CARBOHYD 389 399
FT CARBOHYD 404 404
FT CARBOHYD 453 453
FT VARSPLIC 902 927
FT VARSPLIC 929 941
FT VARIANT 628 628
FT VARIANT 869 869
FT CONFLICT 6 6
FT CONFLICT 12 12
FT CONFLICT 424 424
SQ SEQUENCE 941 AA; 105821 MW; 09F1773DB0673C5D CRC64;

Query Match 15.9%; Score 1066.5; DB 1; Length 941;
Best Local Similarity 29.5%; Pred.No. 6.3e-67;
Matches 270; Conservative 160; Mismatches 340; Indels 145; Gaps 20;

QY 155 LLGLFELSTSRGPRDGLSELGAATMAVEHINKRLPLPGYTLELVNTDCTDPCGVGVDRF 214
DB 58 INGLMPLTKEVAKSGIGRGVLPVAVELAIQIRNESLLRPFYDLRLYDFECDNAKGLKAF 117
QY 215 FHAIYQTPSTRMVMVLGSCSEVTESLAKVPVNNIVQVSVFSGTSPALSDRREFFPYRT 274
DB 118 YDAIKYGNP--HLWFGGVGCPVSTIIAESLQGNLVLQSLFAATTPVLADKKKPYFFRT 175
QY 275 VAPDSSHPARTAFIRKFGCWGITVTFEQNEEVHSLAVNLVLELANISCAATITFA-- 332
DB 176 VESDNAVNPAILKLLKHQYQKRVGTLTQDQVRFSEYRNDLTGVLYGEDIISDTSFSND 235
QY 333 -ATDFKEQLLLREYDTRIIIGSFQSELAPOILCEAYRLRMFCADYAWILHESGAPWPP 391
DB 236 PCTSVKK-----LKGNDVRIILGQFDONMAAKVFCCEAYENMYSKYQWIIPGWYEPSWWE 291

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QY 392 DORT-----ACSNHELOLAVENLIVVSTHNSIVGNVNSYGLNHNMFNSQLRKQSQAFHG 446
DB 292 QVHTEANSSRCLRKLLAAAMEGYI-----GVDFELSSSKQIKTISGTPQOYER 340
QY 447 Q-DGFGSGVGPRIATAATQSDSRRRRRRGVGTSGGHLFPEAISQYAPQTYDAVWAIALA 505
DB 341 EYNNKRSVGP-----SKPHGVAYDGIWIAKT 368
QY 506 LRAAEHRRNEEQSKLDGFDYTRSDMAWEFLQOMKGLHFLGVSGVPSFGDRVGTTF 565
DB 369 LQAMETLHASSRHQRIQDFNTDHTLGRILNANMETNFFGVGTQVVRNGERMCTIKF 428
QY 566 VOIQGLLEPVALYPATDADFRCPRCPVKVHSGQVPIAKRVFKLRVATTAIAFYTI 625
DB 429 TQFQDSREVKVGEYNAVADTLEIIND---TIRFQSEPPKDKTIILEQLRKLSPLYSIL 485
QY 626 ATLSVSGTALATITLAEFLNHFRLKAIKLSLSPKLSNITAVGCFIVYATVILGLDHSITLP 685
DB 486 SALTILGIMIMASAFFNFKRNQKLKRMSSPYMNNLIILGGMLSYASIFLFLDGSFV- 544
QY 686 SAEDSFATVCTARVYLLSAGFSLAFSGFMFAKTYRVHRIFRTGCVFKDKMLQDIQILILV 745
DB 545 -SEKTFETLCVTRWTLVGYTTAFGAMFAKTRVHAIFKNV--KMKKKIIRKQKLLVIV 601
QY 746 GLLLVLDALLVTLVWVTPDMEHLLHNLLEISATRSVVYQPOVEVCRSQHTQWLVSIV 805
DB 602 GGMLLIDLCILICQWQVDPRLRTVEKYSMEPDAGRDISIRPLLEHCENTHMTIWLGIYV 661
QY 806 AVKGLLVGVYMAWETRHVKIPALNDSQYIGSVSVYVITSAIVVLANLISERVTLAF 865
DB 662 AVKGLLMFLGCFLAWETRNVSLPALNDSKYIGMSVYNGVIMCIIGAAVSFLTRDQPNVOF 721
QY 866 ITITALILTSTATLCLLFIPLKDIWARNDIIDPVIHSMGLKMECNTRRFVVDORREIQ 925
DB 722 CIVALLVIFCSTITLCLVFPKL-----ILRTNPDAATQNRREQ 761
QY 926 YRVEQNVYKKEQALDAEIRKLERLESGLTTSTTT--SSSTSLLTG-----GGHLKP 979
DB 762 F---TQNG--KK-----EDSKTSTSVTSVNOASTSRLEGLQSENHRLRM 800
QY 980 ELT-----VTSGISQTPAASK-----NRTPSISG---ILPNLLLS 1011
DB 801 KITELDKLEEVTMOLOQDTPKTTVIKONHYOELNDILNLGNFTSTDDGGKAILKNHL-- 858
QY 1012 VLPVPVIRPWSAE 1026
DB 859 ---DQNPOLQNTTTE 870
RESULT 3
GBRL_HUMAN
ID GBRL_HUMAN STANDARD; PRT: 961 AA.
AC Q9UBS5; Q95375; Q9UQ00; Q96022; Q95975; Q95468;
DF 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GBL1).
GN GABBR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Cerebellum;
RX MEDLINE=99061981; PubMed=9844003;
RA Kaupmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H.,
RA Heid J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
RL expressed and regulate inwardly rectifying K+ channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [2]

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Db 761 F---TQNO--KK-----I-|||I-:|||I-:|||||I-:
QY 980 ELT-----VTSGISQTPAASK-----EDSKTSTSVTSVNOASTSRLEGLOSENHRLRM 799
Db 800 KITELDKLEEVMTQLODTPKTYIKONHYOELNDILSLGNFTSTGGRAILKNHL-- 857
QY 1012 VLPVPVPRASWPSAE 1026
Db 858 ---DQNPQLQWNTTE 869

RESULT 2
GBR2_HUMAN
ID GBR2_HUMAN STANDARD: PRT; 941 AA.
AC Q75899; Q75974; Q75975; Q9UN59; Q9UNR1; Q9P1R2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR
DE 51) (GPR 51) (HG20).
GN GABBR2 OR GPR51.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A. (ISOFORM 2A).
RX TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [2]
RN PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).
RN [3]
RN SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Fetal brain;
RX MEDLINE=99189236; PubMed=10087195;
RA Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA Chateaufneuf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA O'Neill G.P., Liu Q.;
RT "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT receptors expressed predominantly in nervous tissues and mapped
RT proximal to the hereditary sensory neuropathy type 1 locus on
RT chromosome 9.";
RL Genomics 56:288-295(1999).
RN [6]
RN SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC TISSUE=Brain;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface

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RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1.";
RL Mol. Cell. Neurosci. 13:180-191(1999).
RN [7]
RN R1A-R2 INTERACTION.
RX MEDLINE=99175124; PubMed=10075644;
RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA Bonner T.I., O'Neill G.P.;
RT "Identification of a GABAB receptor subunit, gb2, required for
RT functional GABAB receptor activity.";
RL J. Biol. Chem. 274:7607-7610(1999).
RN [8]
RN R1A-R2 INTERACTION.
RX MEDLINE=20237752; PubMed=10773016;
RA Sullivan R., Chateaufneuf A., Coulombe N., Kolakowski L.F. Jr.,
RA Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
RT receptors with truncated receptors and metabotropic glutamate
RT receptor 4 supports the GABA(B) heterodimer as the functional
RT receptor.";
RL J. Pharmacol. Exp. Ther. 293:460-467(2000).
CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTINOCICEPTION.
CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ012188; CAA09942.1; -
DR EMBL; AF056085; AAC63228.1; -
DR EMBL; AF095723; AAC63383.1; -
DR EMBL; AF095724; AAC63384.1; -
DR EMBL; AF095784; AAD30389.1; -
DR EMBL; AF074483; AAD03336.1; -
DR EMBL; AF069755; AAC99345.1; -
DR EMBL; AF099033; AAD45867.1; -

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FT	DOMAIN	712	719	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	720	740	VII (POTENTIAL).
FT	DOMAIN	741	940	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	780	818	COILED COIL (POTENTIAL).
FT	CARBOHYD	89	89	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	403	403	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	452	452	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	19	19	P -> R.
FT	VARIANT	19	19	P -> PP.
FT	VARIANT	337	337	F -> Y.
FT	CONFLICT	343	343	S -> T (IN REF. 2).
SEQ	SEQUENCE	940 AA;	105751 MW;	77BB42D833C7505D CRC64;

Query Match	15.9%;	Score 1068.5;	DB 1;	Length 940;
Best Local Similarity	29.6%;	Pred. No. 4.5e-67;		
Matches 271;	Conservative 159;	Mismatches 340;	Indels 145;	Gaps
Qy	155	LLGLFELSTGRPRDGLSELGAATMAVEHNKRLLPGVTLVLTNDTCQDPGVGVDRF	214	
Db	57	IMGLMPTKKEVAKGISGRGVLPVAVLEIAEQIRNESLLRFLFDLRYDTECNKAGLKAF	116	
Qy	215	PHAIYTOPSTRMVLLGSACSEVTESLAKVPVYNNIVQVSFGSTSPALSDRREFFPYFRT	274	
Db	117	YDAIKYGN - HLMVFGVCPSTYSIIAESLQGNVLQLSFAATTPVLADKKKYPYFFRT	174	
Qy	275	VAPSSHNPIARIATRFKFGMGTVTTFSSQEVHSLAVNLNLTVEAANISCAATITFA -	332	
Db	175	VPSDNVNPAILKLLKHFRRRRVGTLTQDVORESEVRNDLTGVLYGEDIEISDTESFSD	234	
Qy	333	-ATDFKEQLLLRLTDPRIILGFSQSOLAPQILCEAYRLRMFCADYAWILHESMGAPWPP	391	
Db	235	PCTSVKK - - - - LKGNDRVRIILGOLFQDNMAAKVFCCAFESMFSGKYQWITPGWEPAPW	290	
Qy	392	D - - - - QRTACSNHELQALAVENLIVSTHNSIVGNVYSGLNHHMFNSOLRKQSAQFH	446	
Db	291	QVHVEANSSRCLRSLLAMEGYI - - - - -GVDFEPLSKQIKTISGKTPOOFR	339	
Qy	447	Q - DQFGSGYGPRTSIATQSDSRRRRRRGVGTSGGLHPEATISQYAPQTYDAVNAIALA	505	
Db	340	EYNSKRSGVGP - - - - -SKPHGYAYDGIWVIATK	367	
Qy	506	LRAAEHWRNEQSKLDGPDYTRSDMAWEFLOQMGLHFLGVSGPVSESGPDRVCTTAF	565	
Db	368	LQRAWETLHASSRQRIOEDNYDHTLGLKILLNAMNETNFFGVGTQGVFRNEMRGMTIKF	427	
Qy	566	YQIQGLLEPVALYPATDALDFRCPRCPVKVHSGQVPIAKRVFKRLVATAPLAFYTI	625	
Db	428	TQFODSREVKGVEYNADVTLLEIND - - - - -TIRQGSPEPKDKTIIILEQLRKISLPLSYL	484	
Qy	626	ATLSVSGIALAITFLANLHFRKLKAIKLSPPKLSNITAVGCITFYVAVILGLDHSHTLP	685	
Db	485	SALTILGIMIASAFLENKRNQKLIKMSPPYMNLIILGGMLSYASIFLDFELGDSFV -	543	
Qy	686	SAEDSFATVCTARYVLLSAGFSLAFSGFMFAKTVRVHRIPTRTGSPVKMKMODIQLILV	745	
Db	544	-SEKTFETLCTRWITLVGYTAFGAMFAKTVRHAIFKNV - - - - -KMKKIIIIKDQKLLIV	600	
Qy	746	GLGLLVALLVTLVWVTDPMERHLNLTLEISATDRSVVYQPOVEYCRSHQTOFWLSVLY	805	
Db	601	GGMLLIDLCILCQAVDPLRRVVERYSMPDPAGRDIISIRPLEHCENHTHWILGIVY	660	
Qy	806	AYKGLLVGVYMAWETRRHYKIPALNDSQYIGSVYSVVTISAIVVVLVANLISERVTLAF	865	
Db	661	AYKGLLMFCFLAWETRNYSIPALNDSKYIGSVYVNGIMCIIGAASVFLRDQPNQVF	720	
Qy	866	ITTALLTSTTATLCLLFTPKLHDITWARNDIIDPVIHSMGLMKMCEKNTRRFVVDORRELQ	925	
Db	721	CIVALVYIIFCSTILCLVFPKL - - - - -ITLRTNPDAATNRRRQ	760	
Qy	926	YRVEVONRVYKFTOALDAFTIKLERILPESGLTDTTSTTP - - - - -SSSTSLINCG - - - - -GGHKKP	979	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:08:01 ; Search time 24.07 Seconds
(without alignments)
1987.852 Million cell updates/sec

Title: US-09-715-962-6
Perfect score: 6705
Sequence: 1 MRIIQPVQTRYGPWPVAVGL.....RLSLGDSQEEQQAPANGTE 1305

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1068.5	15.9	940	1 GBR2_RAT	O88871 rattus norv
2	1066.5	15.9	941	1 GBR2_HUMAN	O75899 homo sapien
3	991.5	14.8	961	1 GBR1_HUMAN	Q9ubs5 homo sapien
4	990.5	14.8	960	1 GBR1_MOUSE	Q9wv18 mus musculu
5	971.5	14.5	991	1 GBR1_RAT	Q920u4 rattus norv
6	372	5.5	877	1 MGR6_HUMAN	O15303 homo sapien
7	367	5.5	871	1 MGR6_RAT	P35349 rattus norv
8	349.5	5.2	872	1 MGR2_HUMAN	Q14416 homo sapien
9	349.5	5.2	915	1 MGR7_HUMAN	O14831 homo sapien
10	348.5	5.2	915	1 MGR7_RAT	P35400 rattus norv
11	347	5.2	912	1 MGR4_HUMAN	Q14833 homo sapien
12	343.5	5.1	872	1 MGR2_RAT	P31421 rattus norv
13	343	5.1	879	1 MGR3_RAT	P31422 rattus norv
14	339.5	5.1	908	1 MGR8_RAT	P70579 rattus norv
15	337.5	5.0	908	1 MGR8_HUMAN	O00222 homo sapien
16	336.5	5.0	908	1 MGR8_MOUSE	P47743 mus musculu
17	336	5.0	912	1 MGR4_RAT	P31423 rattus norv
18	330	4.8	877	1 MGR3_HUMAN	Q14832 homo sapien
19	306.5	4.6	976	1 MGR_DROME	P91685 drosophila
20	306.5	4.6	999	1 MGR1_CAEEL	Q09630 caenorhabdi
21	257.5	3.8	1199	1 MGR1_RAT	P23385 rattus norv
22	257	3.8	1203	1 MGR5_RAT	P31424 rattus norv
23	242	3.6	1194	1 MGR1_HUMAN	Q13255 homo sapien
24	240	3.6	1085	1 CASR_BOVIN	P35384 bos taurus
25	237	3.5	1078	1 CASR_HUMAN	P41180 homo sapien
26	230.5	3.4	1079	1 CASR_MOUSE	Q9qy96 mus musculu
27	223.5	3.3	1212	1 MGR5_HUMAN	P41594 homo sapien
28	221.5	3.3	1079	1 CASR_RAT	P48442 rattus norv
29	166.5	2.5	1047	1 ANPB_BOVIN	P46197 bos taurus
30	166.5	2.5	1047	1 ANPB_RAT	P16067 rattus norv
31	162.5	2.4	1047	1 ANPB_HUMAN	P20594 homo sapien
32	160	2.4	847	1 MMLB_STRCO	O54101 streptomyce
33	137	2.0	369	1 LIVK_ECOLI	P04816 escherichia

RESULT 1

GBR2_RAT ID	GBR2_RAT STANDARD;	PRT;	940 AA.
AC O88871; Q9QWU2; Q9JK36;			
DT 20-AUG-2001 (Rel. 40, Created)			
DT 20-AUG-2001 (Rel. 40, Last sequence update)			
DT 20-AUG-2001 (Rel. 40, Last annotation update)			
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).			
GN GABBR2.			
OS Rattus norvegicus (Rat).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX NCBI_TaxID=10116;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Hypothalamus;			
RX MEDLINE=99087320; PubMed=9872315;			
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M., Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q., Salton J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A., Branchek T.A., Gerald C.;			
RA "GABA(B) receptors function as a heteromeric assembly of the subunits GABA(B)R1 and GABA(B)R2.";			
RT Nature 396:674-679(1998).			
RL [2]			
RN SEQUENCE FROM N.A.			
RP TISSUE=Brain cortex, and Cerebellum;			
RX MEDLINE=99087322; PubMed=9872317;			
RA Kaupmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P., Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A., Bettler B.;			
RT "GABA-B receptor subtypes assemble into functional heteromeric complexes.";			
RL Nature 396:683-687(1998).			
RN [3]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Brain cortex;			
RX MEDLINE=20193514; PubMed=10727622;			
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;			
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";			
RL Brain Res. 860:41-52(2000).			
RN [4]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Hypothalamus;			
RP Borowsky B., Laz T., Gerald C.;			
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RL [5]			
RP RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.			
RC TISSUE=Hippocampus;			
RX MEDLINE=99102694; PubMed=9872744;			
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A., Kornau H.-C.;			
RT "Role of Heteromer Formation in GABA-B Receptor Function.";			
RL Science 283:74-77(1999).			
CC -I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS			

34	133.5	2.0	369	1	LIVK_SALTY	P17216 salmonella
35	133	2.0	537	1	ANPC_BOVIN	P10730 bos taurus
36	132.5	2.0	1687	1	VIT2_FUNHE	Q98893 fundulus he
37	131.5	2.0	540	1	ANPC_HUMAN	P17342 homo sapien
38	130.5	1.9	536	1	ANPC_MOUSE	P70180 mus musculu
39	130.5	1.9	722	1	HMN2_DROME	P22808 drosophila
40	127	1.9	821	1	ALGI_HUMAN	Q43747 homo sapien
41	125.5	1.9	2300	1	CYAA_NEUCR	O01631 neurospora
42	123.5	1.8	1113	1	HDA5_MOUSE	Q92246 mus musculu
43	122.5	1.8	2167	1	BEM2_YEAST	P39960 saccharomyc
44	122	1.8	535	1	ANPC_RAT	P41740 rattus norv
45	121.5	1.8	565	1	SCRI_SCHPO	O14335 schizosacch

ALIGNMENTS

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE GLU-RA PROTEIN.
 GN GLU-RA OR CG11144.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielson A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siding A.C., Stappleton M., Strong R., Sun E.,
 RA Spier E., Spradling A.C., Stappleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith L.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AF003846; AAF59402.1; .
 DR FlyBase: FBgn001985; Glu-RA.
 DR InterPro: IPR001828; ANF_receptor.
 DR InterPro: IPR000337; GPCR_Mgr.
 DR Pfam: PF00003; 7tm_3; 1.
 DR Pfam: PF01094; ANF_receptor; 1.
 DR PRINTS: PR00248; GPCRGR.
 DR PROSITE: PS00979; G_PROTEIN_RECF3_1; 1.
 DR PROSITE: PS00980; G_PROTEIN_RECF3_2; 1.
 DR PROSITE: PS00981; G_PROTEIN_RECF3_3; 1.
 DR PROSITE: PS0259; G_PROTEIN_RECF3_4; 1.
 DR PROSITE: PS0259; G_PROTEIN_RECF3_4; 1.
 SQ SEQUENCE 976 AA; 108485 MW; 43A0E1F918EDACC4 CRC64;

Query Match 4.6%; Score 307.5; DB 5; Length 976;
 Best Local Similarity 19.9%; Pred. No. 6.1e-14;
 Matches 202; Conservative 147; Mismatches 342; Indels 323; Gaps 47;

QY 151 GKIVLLGLLEL-----STSRGPR--PDGSELGAATMAVEHINR-KRLLPGYTL----- 196
 DB 43 GDIIILGLFPVHEKRGAPCGPKVYRNGVQRLEAMLYAIDRVNNDPNILPGITIGVHILD 102

QY 197 -----ELVTNDTQCDPCGVGVDREFFHAIYTOPSTR-----MVM 228
 DB 103 TCSRDYALNQSILQFVRASLNNLDTSGYECADG-----SSPQLRKNASSGPVFG 151
 QY 229 LLGSACSEVTESIAKVVPYWNIVOVSGSTSPALSRRREFFPYRYTVAPDSSHNPARIAF 288
 DB 152 VIGGSYSSVSLQVANLRLHFHPQVSPASTKLTSLKTRFDLRFARTVPPDFTOSVALVDI 211
 QY 289 IRKFGWGTVTTFESQNEEVHSLAVNNLVTELEAAN--ISCAATITFAATD--FREQL-LLL 343
 DB 212 LANFNWSYVSTIHSEGSYGEYGEALHKEATERNVCIKVAEKVPSAADDKVFIISIKLQ 271
 QY 344 RETDRIIIGTSFQELAPOLICEAYRLRMFGADYANILHESMGAPMWPQORTACSNHELO 403
 DB 272 KPNARGVVLFTRAEDARRILOAKRANL--SOPFHWIASDG-----WGKQOKLL---EGLE 323
 QY 404 LAVENLVVSTHNSIVGN-----NVSYSGLNNHMFNSQLRKSQAQPHQGD 448
 DB 324 DIAEGAITVELOSEIIADFDRYNNMQLTPTETNORNPFAEYWEWDTFNCVLTSLSVK----- 378
 QY 449 GFSGYGPRIISIAAATQDSR-----RRRRRGVVGTSGGHLFPPEAISQYAPQTYD 497
 DB 379 -----PPTSANSSTDNKIGVKAKTECDDSYRLSEKVGYE-----QESKTOF---VVD 423
 QY 498 AVMAIALRAAAEEHWRNEEQSKLDGFDYTRSDMAW-----E 535
 DB 424 AVYAFAYALHNLHNDRCNTQSDQTTETRKHLOSEVWYRKISTDTKSOACPDMDYDGE 483
 QY 536 FLQO-MGKLHFLGVSG-PVPSGSPDRVG-----TFAYQIQ-----RGL 572
 DB 484 FYNNYLLNVSFIDLAGSEYKF---DRQDGLARYDILNYORQENSSGYQVKGKWFNGL 540
 QY 573 L-----BPV-ALYYPATDAL-----DFRCPCR 594
 DB 541 QLNSETVVMWNETEQTSACSIPCEVGMKIKQOGDTCCWICDSCSEFEVYDEFTCKDGG 600
 QY 595 P-----VKWHS--GOVPIAKRVKRLVATIAPIAFYTIATLTSVGLA 634
 DB 601 PGLWPYADKLSCYALDIQYMKWNSLFAIPMAIIF-----GIA 639
 QY 635 LAITFLAFNLHFRKKAIAKLSPPKLSNITAVGCFVYATVILLGLDHSHTLPSAEDSFATV 694
 DB 640 LFSIVIVLFAKNHDTPLVRASGRELSYTLFGILVCYCNFTAL-IAKPTIGS----- 690
 QY 695 CTARYLLSAGFSLAGSMFAKTYRVHRIF-TRTGSVEFKDKMLQDIQLILLGGLLVDA 753
 DB 691 CVLQRFQGVGFSIIYSALLTNTNLSRIFHSASQAQRKYISPOSQVVTSLIAIOV 750
 QY 754 LVLTLWVYDTPMERHLNLTLEISATDRSVVYQPVQVEV---CRSQHTQTLWSLYIA--YK 808
 DB 751 LITMIWVVEPPGTRFY-----YPRDRREVILCKIQD---MSFLFSQLYN 792
 QY 809 GULLVGVYMAWETHRVKIPA-LNDSQYIGSVYSV-VITSALVVV---LANLISERVTL 863
 DB 793 MILITICTIYAIKTR--KIPENFNESKFGFTMYTTCIIILAFVPIYFGTGSYEVQTTT 850
 QY 864 AFITITALILTSTTATLCLEFPLKLDIWARNDIIDPVTHSMGLKMECTRFREVVDDRE 923
 DB 851 LCISIS---LSASVALVC-LYSPKVYIL-----VFHP-----DKNVRKLTMN----- 888
 QY 924 LQYRVEQNVYKKEIQALDAEIRKLERLLESGLATT-----STTSSSTSLTGG 974
 DB 889 -----STVYRRSAAA-----VAQGAPTISSGYSRTHAPGTSALITGG 923
 RESULT 15
 Q93564
 ID Q93564 PRELIMINARY; PRT: 1267 AA.
 AC Q93564; Q93728;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

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QY 448 DG-----FGSGYGRPRISIAATQSDSRRRRGVGTSGGHLFPPEAISQVAPQTYDA 498
Db 448 KGADSIKVEDTYGDGNG-RYNNFQHIGGKYSYLK-----GH-----485
QY 499 VWAIALALRAAEHWRNEQSKLDGFDYTRSDMAWEFLQOMGKHLFLGVGSPVSPGPD 558
Db 486 -WAETLYLDVDSIHSRN-----SVPTS-QCSD 511
QY 559 RVGTAFYQIQRG-----LLEPVALYYPATDADFRCPRCPVKWH-----SGOVPIAKRV 609
Db 512 PCAPNEMKMGPDVCCVICPEYEVLD--EFTCMDCGPGQWPTADLSGCGYNLPEDY 569
QY 610 FKLRA-TIAPLAFYTIATLSVGTALAIT-FLAPNLHPRKKAIAKLSPKLSNITAVGC 667
Db 570 IRWEDAWAIGPV--TIACLGFMCTCIVITVFIKH-----NTPLVKASGRELCYIILLFGV 622
QY 668 IFVYATVILLGLDHTLPSAEDSFATCTARVYLLSAGFLAFSGFMFAKTYRVHRIF--T 725
Db 623 SLSCYMTFF-----IAKFS-----PVCALRLGLGTSFAICYSAULTTNCIARIFDGV 673
QY 726 RTGSVFKDKMLQDIOILILVGLLVDALLVTLWVTPDPMERHLHNLTLLEISATDRSVVY 785
Db 674 KNGAQ-RPKFISPSQVFCGLGLILVQIMVSWILI-----LETPCTRYTLP 720
QY 786 QPOVEV-----CRSQHTQTMVSVLYAYKGLLVGVYVMWETRVHKIPA-LNDSOYIGSVY 841
Db 721 EKRETVILKCNVKDSMLISL--TYDVLVILCTVYAEKTR--KCPENFNKAFIGFTMY 776
QY 842 SVWITSATVVVLANLISERVTLAFITILITST-----TATLCL-----LF 884
Db 777 TTCI-----IWLAFUPI--FYVTSSDYRVQTTMCTISVLSGFWVLGCLF 819
QY 885 IPKLHDIWARNDIIDPVHSMGLMEKCNTRFVDDRELQYRVEYQNVKKEIQALDA 944
Db 820 APKVHIV-----LFQP-----QXNV-YTHRLH-----840
QY 945 EIRKLERLESGLTTSTTTSTSTSLT 972
Db 841 ----LNRFSSVSGTATTYSOSSASTYVPT 864

RESULT 13
Q9PWE1 ID Q9PWE1 PRELIMINARY; PRT; 977 AA.
AC Q9PWE1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR (FRAGMENT).
GN GLUR.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA;
RA Hellmich H.L., Micci A.M., Sanchez X., Christensen B.N.;
RT "Molecular cloning, functional expression and localization of a novel
RT metabotropic glutamate receptor linked to calcium mobilization from
RL the catfish retina."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076473; AAD47893.1;
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR001828; ANF_receptor.
DR Pfam: PF01094; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PROSITE: PS00979; G-PROTEIN_RECEP_F3_1; 1.
DR PROSITE: PS00981; G-PROTEIN_RECEP_F3_3; 1.
DR PROSITE: PS50259; G-PROTEIN_RECEP_F3_4; 1.
KW Receptor.
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FT NON_TER 977 977
SQ SEQUENCE 977 AA; 108759 MW; BD06A67E240751CE CRC64;

Query Match 4.6%; Score 311.5; DB 13; Length 977;
Best Local Similarity 20.7%; Pred. No. 3.1e-14;
Matches 181; Conservative 129; Mismatches 342; Indels 221; Gaps 33;

QY 141 MSPAEMORNH-----GKIVLLGLFELSTSRGP-----RPDGLSELGAATMAV 182
Db 38 VSPALMAHOHTPHSIRKIPDVTGLGLFPVH-SKGPLQACGEIKKEKGVHRMEAMLYAL 96
QY 183 EHINR-KRLLPGYTL-----ELVTNDQCPDPGVGVDRFF 215
Db 97 DQINSDELLPNITLRTILDTCSDRTYALRQSLTFVQALIKQKDTSDIRCSNGE-----150
QY 216 HAIYQSTRMVMLLSACSEVTESLAKVVPYWNIVQVSFGSTSPALSDREFFPYFRTV 275
Db 151 OPTIRKPE-RVVGIVGASASSVIMVANVLRLEIPOISYASTAPELSDNNRNYDFSrv 209
QY 276 APSSSHNPARIATIRKFGWGTVTTFQNEEVHSLAVNNLV-TELEAANISCAATITFAAT 334
Db 210 PPDYQQAQAVDIYKALGNVYFIFILASGNTGESVDFAVQISREAGGLCIAQSMKIPRD 269
QY 335 ----DFKEQLLLRET-DTRIIIGFSQELAPQILCEAYRLRMFGADYAMILHESMGAPW 389
Db 270 PKGFEKIIKRLMETPNARGIILIFANEDDIKQVLEAARRANLTG-HFKFVGSDSWGAKS 328
QY 390 WPDORTACSNHELQALAVENLIVSTHNSIVGNVNNYSYSLNNHMFNSQLRKQSAQPHGQDG 449
Db 329 AP-----ILDNEEVAEGAVTILPKRASVEGFDQYFTRSLNRRNRNITWFAEF 375
QY 450 FGSYGPRISIAATQSDSRRRRGVGTSGGHLFPPEAISQVAPQ-----TYDAYVA 501
Db 376 WEDDFCKLTPGKLDPEKKKCTG-----KERIGRSPYEQEGKVQVDAIYVA 425
QY 502 IALALRAAEHWRNE-----EQSKLDG---FDYTRSDMAWEFLQOMG-----541
Db 426 MAHALHNNHQTCARGRTCKMDPVEGRLLLSYTR--AVNFNGSAGTGVLFNENGADPG 482
QY 542 ----KLHFLGVSGP-----VSFGPDRVGTTFAYQI-----QRLLEPAL-----578
Db 483 RYDIFQYQFNTSSPGYKVGOSFSISSAKTSSPGYKVGOWTNLNGINEVEEQMSGGE 542
QY 579 -YYPATDALDFRC--PRCPVK-----WHS-----GOVPIAKRVFKLRVATIAP 619
Db 543 HYIPAS-VCSPQCPQGERKKMVGVPCCWHCEPCDGYQYQVGEITCEMCPFDMR-----P 596
QY 620 LAFYTIAT-----LSSVGIALAITFLAFNLHFRKLKAIKLSPPKLS 660
Db 597 TANTHTACTPTPIIKLDWHSWAVVPMFLAILGIAATLSVIVFVRFNDTPIVRASGRELS 656
QY 661 NITAVGCIFFVYATVILLGLDHTLPSAEDSFATCTARVYLLSAGFLAFSGFMFAKTYRV 720
Db 657 YVLLTGIFLYILITFLMTAEPNTV-----VCALRRLLLGLGMCITYSAMLTKTNRI 707
QY 721 HRIETP-TGSVFKDKMLQDIOILILVGLLVDALLVTLWVTPDPMERHLHNLTLLEISAT 779
Db 708 YRIFEQKKSVTAPKFIPTSQLVITFVSVFQVIGVFIWFGVVPDH-----TIV 757
QY 780 DRVVYQPOQVECVRS-----QHTQWLSVLYAYKGLLVGVYVMWETRVHKIPALNDSQY 835
Db 758 DYDELPPNPPELARGILKCDMSDLSLICLSYSILLMTCTVYAVKSGVP-ETFNEAKP 816
QY 836 IGVSVSVVITSAIVVVLANLISERVTLAFITI 868
Db 817 IGFTWYTTCTI-----VWLAFVPI 834

RESULT 14
Q9V485 ID Q9V485 PRELIMINARY; PRT; 976 AA.
AC Q9V485;
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DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCR_MGR.
DR PROSITE: PS00979; G_PROTEIN_RECEPT_F3_1; 1.
DR PROSITE: PS00980; G_PROTEIN_RECEPT_F3_2; 1.
DR PROSITE: PS00981; G_PROTEIN_RECEPT_F3_3; 1.
DR PROSITE: PS00982; G_PROTEIN_RECEPT_F3_4; 1.
DR PROSITE: PS02059; G_PROTEIN_RECEPT_F3_4; 1.
DR SEQUENCE 983 AA; 109276 MW; 072F0D8B3A840A80 CRC64;

Query Match      5.0%; Score 336; DB 11; Length 983;
Best Local Similarity 22.1%; Pred. No. 4.7e-16;
Matches 193; Conservative 134; Mismatches 346; Indels 200; Gaps 36;

QY 148 RNHGKIVLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLPLPGVTLE 197
DB 148 RHHGKIVLGLFELSTSRG-----PRPDGLSELGAATMAVEHINR-KRLPLPGVTLE 197
DB 44 RIDGDITLGLFVH-GRGSEKAGKELKEGHRLEAMLFALDRINNDPDLPLNITLG 102
QY 198 LVNTDQCDPGVGVDRFFHA-----LYTQPSTRMVMALL 230
DB 198 LVNTDQCDPGVGVDRFFHA-----LYTQPSTRMVMALL 230
DB 103 ARILDT-----CSRDTHALEQSLTFVRALIEKDGTEVRCGGGPPPIITKPE-RVVGVI 154
QY 231 GSACSEVTESLAKVVPWNIVQVSGFSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIR 290
DB 231 GSACSEVTESLAKVVPWNIVQVSGFSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIR 290
DB 155 GASGSSVSIWANILRLFKIPQISYASTADPLSDNSRYDFRSVVPDITYQAQAMVDIVR 214
QY 291 KFGWGVTFTTSONEEVHSLAVNNLVTE-LEAANISCAATITF-----AATDFKEQLLLRE 345
DB 291 KFGWGVTFTTSONEEVHSLAVNNLVTE-LEAANISCAATITF-----AATDFKEQLLLRE 345
DB 215 ALKNWVSTLASEGSGVEAFIQKSRENGGVCIQAQVKIPREPKTGEFKIIRLLE 274
QY 346 TDTRIIIGSFQELAPQILCEAYLRMFGADYAWILHESMGAPWPPORTACSNHEQLOLA 405
DB 346 TDTRIIIGSFQELAPQILCEAYLRMFGADYAWILHESMGAPWPPORTACSNHEQLOLA 405
DB 275 TSNARGIIFANEDDIRRVLEAARRANQTGHFFWMSDSWGSKSAPVLR-----LEEY 327
QY 406 VENLIVVSTHNSIVGNVSYGLNNHMFNSOLRKSQAQFHCQDGFSGYGRISAIATQS 465
DB 406 VENLIVVSTHNSIVGNVSYGLNNHMFNSOLRKSQAQFHCQDGFSGYGRISAIATQS 465
DB 328 AGAV-----TILPKRMVGRFDRFYESSRTLDNRRNIWFAEFWDNFCKLSRHALK 381
QY 466 DSRRRR--RRGVVGTSGHFLFPAISQYAPQTYDAVMAIALARAPEHW--RRNEPQSK 521
DB 466 DSRRRR--RRGVVGTSGHFLFPAISQYAPQTYDAVMAIALARAPEHW--RRNEPQSK 521
DB 382 GSHIKKCTNRERIGQDSAY-EQEGKVQF---VIDAVYAMGHALHAMHRDLCPGRVGLCPR 437
QY 522 LDGFDYTRSDMAWEFLQOMKGLHFLGVSG-PVSFS-GPDVRGTTAFYQIORGLLEPVALLY 579
DB 522 LDGFDYTRSDMAWEFLQOMKGLHFLGVSG-PVSFS-GPDVRGTTAFYQIORGLLEPVALLY 579
DB 438 MDPVDTG-----QLLKYIRNWFNSGIAGNPVTNENGAPGRYDIYQYQ---LRNGSAE 488
QY 580 YPA---TDALDFRCPR-----CRP-----VK-----WH----- 599
DB 580 YPA---TDALDFRCPR-----CRP-----VK-----WH----- 599
DB 489 YKVGISWTDLHLRIERMQWPGSGQQLPRISICSLPCQPGERKKTVMGMACCWCEPCTGY 548
QY 600 -----SQGVPIAKRVFKLRVATIAPLAFYTTIATLSSVGIA- 634
DB 600 -----SQGVPIAKRVFKLRVATIAPLAFYTTIATLSSVGIA- 634
DB 549 QYQVDRTCTCPYDMRPTENRTSCQPIPIVKLEWDSPPA-VLPL-----FLAVVGIAA 601
QY 635 ---LAITFLAFNLHFKLKAALKSLKSNITAVGCFIVATVILLGLDHSITLPSAEDSF 691
DB 635 ---LAITFLAFNLHFKLKAALKSLKSNITAVGCFIVATVILLGLDHSITLPSAEDSF 691
DB 602 TLFVVVTVFRYN---DTPIVKASGRELVSYVLAGIFLCVATFLM-----IAEPDL 649
QY 692 ATVCTARVLLSAGSFLAFSGFAKTYVRHRIETR-TGSVFKDKMLQDIOILLVGLLL 750
DB 692 ATVCTARVLLSAGSFLAFSGFAKTYVRHRIETR-TGSVFKDKMLQDIOILLVGLLL 750
DB 650 GT-CSLRIRIFLGLMSISYAALLTKNRIYRIFEQGKRSVSPRFPSPASQLAITFLIS 708
QY 751 VDALLVTLWVVDTPMERHLNLTLEISATDRSVV-YQPOVE-----VCRSOHTOTWL 801
DB 751 VDALLVTLWVVDTPMERHLNLTLEISATDRSVV-YQPOVE-----VCRSOHTOTWL 801
DB 709 LQLLGICVWFVVDP-----SHSVVDQDQDTLDRFARGVLKCDISL 753
QY 802 SVLYAYKGLLLVGVVWAMETHRVKTPALNDSQYIGSVSV-VITSADVVL--ANLIS 858
DB 802 SVLYAYKGLLLVGVVWAMETHRVKTPALNDSQYIGSVSV-VITSADVVL--ANLIS 858
DB 754 ICLLYSMLLMTCTVYAIKTRGP-ETENEAKPIGFTMTYTCIVWLAFIPFEGTSOSA 812
QY 859 ERVTLAFITITALILTSTATLCLLFIPLKLDI 891
DB 813 DKLYIQTTLTVSVLSASVSLGMLYMPKVYII 845
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RESULT 12
QYQYS2
ID QYQYS2 PRELIMINARY; PRT; 879 AA.
AC QYQYS2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 3 PROTEIN.
GN GRM3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RC SEQUENCE FROM N.A.
RP STRAIN=129/SV;
RX MEDLINE=20012997; PubMed=10544282;
RA Minoshima T., Nakanishi S.;
RT "Structural organization of the mouse metabotropic glutamate receptor
RT subtype 3 and its regulation by growth factors in cultured cortical
RT astrocytes."
RL J. Biochem. 126:889-896(1999).
DR EMBL; AF170701; AAF06741.1; -.
DR EMBL; AF170697; AAF06741.1; JOINED.
DR EMBL; AF170698; AAF06741.1; JOINED.
DR EMBL; AF170699; AAF06741.1; JOINED.
DR EMBL; AF170700; AAF06741.1; JOINED.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEPT_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEPT_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEPT_F3_3; 1.
DR PROSITE; PS02059; G_PROTEIN_RECEPT_F3_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 879 AA; 99113 MW; F3A8B26CE96679EF CRC64;
```

Query Match 4.9%; Score 329; DB 11; Length 879;
Best Local Similarity 19.9%; Pred. No. 1.3e-15;
Matches 197; Conservative 133; Mismatches 332; Indels 326; Gaps 44;

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QY 151 GKIVLLGLFELS-----TSRGRPDGLSELGAATMAVEHINRKR-LLPG-----YTL 196
DB 151 GKIVLLGLFELS-----TSRGRPDGLSELGAATMAVEHINRKR-LLPG-----YTL 196
DB 37 GDLVIGLGLFIPINEKGTGTECGRINEDRGIRQLEAMLFADINKNYLLPGVKLGVLHIL 96
QY 197 ELVTNDT-----QCDPGVGVDVDFHAIYTPQSTRMVLIGSAC 234
DB 197 ELVTNDT-----QCDPGVGVDVDFHAIYTPQSTRMVLIGSAC 234
DB 97 DTCSDRTVALEQSLFVFRASLTKVDEAEVPCPDG-----SYAIQENIPLLIAGVIGSY 150
QY 235 SEVTESLAKVVPWNIVQVSGFSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIRKFGW 294
DB 235 SEVTESLAKVVPWNIVQVSGFSTSPALSDRRFFPYFRTVAPDSSHNPARIAFIRKFGW 294
DB 151 SSVSTQVANLLRFQIPQISYASTSAKLSKSDKSYDYFARTVPPDFYQAKAMAEILRYFNW 210
QY 295 GTVTTFSONEEVHSLAVNNLVTELEAANISCAATITFAATDFKEQL-----LLLRETDR 349
DB 295 GTVTTFSONEEVHSLAVNNLVTELEAANISCAATITFAATDFKEQL-----LLLRETDR 349
DB 211 TVSTVASEGYGETGIEAFQEARLNRICITAEKVGSRNIRKSYDSVIRELQKPNAR 270
QY 350 IIGSFSQELAPQILCEAYLRMFGADYAWILHESMGA----- 387
DB 350 IIGSFSQELAPQILCEAYLRMFGADYAWILHESMGA----- 387
DB 271 VVVLFMRSDDSDRELIAAASRV---NASFTWASDQWGAGQESIVKGESEHVAYCAITLELAS 327
QY 388 -----PWPDP---QRTACS-----NH-----ELQAYE----- 407
DB 388 -----PWPDP---QRTACS-----NH-----ELQAYE----- 407
DB 328 HPVRQFDRYFQSLNPYNHNRPNWPRDFWEQKFQCSLQNKRNHRQICDKHLAIDSSNYEQE 387
QY 408 -----NLIVVSTH-----NSIVGNVSYGLNNHMFNSOLRKO-----SAQFHQ 447
DB 408 -----NLIVVSTH-----NSIVGNVSYGLNNHMFNSOLRKO-----SAQFHQ 447
DB 388 SKIMEVNVAVYAMAHALKMORTLCPTNTTKCDAMKILDGKKLYDKYLLKINFTAPFPNP 447
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QY 595 PVKWHSG---QVPIAKRVFLRVATIA-PLAFYTIATLSSVGVIALATFLAFNLFHFKL 649
Db 113 PGMPDGIPINDGIDIE-----NVTVSPLTVVVA-LAVGLVFAIVCFEFTVIERKR 165
QY 650 KAILKSPKLSNITAVGICFYATVILGLDHSSTLPSAEDSFATV-CTARVYLLSAGFSL 708
Db 166 KLIRLSPFNLYLGLGAILIYFNVITL-----VPTTDTVIAAILCNINPWLTSGLYSL 220
QY 709 AFGSMFAKTVRVHRIFT--RTGSGFKMDQIDQILVGLLGLLDVALLVTLVWVYDPM 766
Db 221 CYGTILAKTIRIWFENKPRVPSVTKSIVIKDYALALFWSLVWIDVILIGLFAIVEGLR 280
QY 767 RHL-----HNLTEISATDRSVYQPOVEVCRSHTQTLVSLVYAYKGLLLVGVYVWAM 820
Db 281 GELAVHRTSNKENIEDTIGPTCEFHQYLYICKSKGOVALETVLFYKGLLQVTLILAF 340
QY 821 ETRHVKIPALNDSOYIGVSYSVVTSAIVVLANLISERVTLAFITITALTITSTTATL 880
Db 341 NTRKVKVGLDSDSYIAAAIYVTSILVAAISTVTLRDYVNIYPVAVGIGFLGTTMIL 400
QY 881 CLLFIPKLHDIWARNDIIDPVIHSMGLKMECNTRRFVVD--DRRELQYRVEQVNRVKKRI 939
Db 401 GLVFPVRMVGLYQ-----DP-----QGDNIKISNSHSHDVPDRDSAYSPDAEIRLKORI 451
QY 940 QALDAEIRKLERLESGLTTSTTSSS 967
Db 452 SELEKNIQ-----PSOMFPMGTTSVS 473

RESULT 10
Q9H3N6 PRELIMINARY; PRT; 872 AA.
AC Q9H3N6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR TYPE 2.
GN HMG2LUR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasuyuki F., Akiko J.;
RT "Structure and polymorphisms of the human metabotropic glutamate
RT receptor type 2 (hmg2lur2) gene : Analysis of association with
RT schizophrenia."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB045011; BAB19817.1; -.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR PRINTS; PF01094; ANF_receptor; 1.
DR PROSITE; PS00248; GPCR_MGR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 872 AA; 95567 MW; 801976D034AA8100 CRC64;

Query Match 5.2%; Score 350.5; DB 4; Length 872;
Best Local Similarity 21.9%; Pred. No. 3.2e-17;
Matches 193; Conservative 112; Mismatches 343; Indels 233; Gaps 35;

QY 151 GKIVLGLFELSTSRGPRPD-----GLSELGAATMAVEHINR-KRLLPG----- 193
Db 30 GDVLVGLGLFPVHQKQPAEDCPVNEHRIQRIEAMLFALDRINRDPHLLPGVRLGAHIL 89
QY 194 -----YTLVNTDTCQDGVGVDRFRH-----AIYTOPSTRMWMLLGSACEVTE 239
Db 90 DSCSKDTHALBQALDFVRASLSRGADGSRHRICPDGSIYATHGAPTAITGVIGGYSDSVI 149
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QY 240 SLAKVVPYNNIVQVSGSTSPALSDRRFPYFYRTVTVAPDSSHNDPARIATIRKFGWGTVT 299
Db 150 QVANLRLFOIPQISYASTSAKLSKSRDYFARTYPPDFFOAKAMAEILRFFNWTYVST 209
QY 300 FSONEVEHSLAVNNLVTELEAANISCAATI-----TEAATDFKEOL-LLLRETDTRIIG 353
Db 210 VASEGDTGETGIEAFELEARNI-CVATSEKVGGRAMSRAAFEGVVRALLQKPSARVAVL 268
QY 354 SFSEOLAPQILCEAYRLRMFGADYAWILHESMGA-----PW-----WPDQRTACSNHIELOAVENLIV 387
Db 269 FTSSEDARELLAASQRL--NASFTWVASDGVGALESVAGSEGAEGAITIELASYPIS 325
QY 388 -----STHNSIVGNVYSYSLNNHMFNSQLRKSAQFHGQDGFSGVGPRISTAAT 412
Db 326 DFASYFQSLDPWNNSRNPWFREFW-EQRFRCFSRQRDCAAHSLRAVPFQESKIMFVNVA 384
QY 413 -----STHNSIVGNVYSYSLNNHMFNSQLRKSAQFHGQDGFSGVGPRISTAAT 463
Db 385 VYAMAHALHMHKALCNPNTTTLCDAMPVNGRRLYK---DFVLNVKFDAPFRP-----ADT 437
QY 464 QDSRRRRRRGVVGTSGGHLFPPEAISQYAPQTVDAVWAIALALAAEHEHRRNEEQSKLD 523
Db 438 HNEVRDR-----FGDIGRYNIFTY-----LRAGSRVYQKGVYAAE 476
QY 524 GFDYTRSDMAWEFLQOMKGLHFLGVSGPVSFSG-----PDRVGTTFAYQIQRGLLEPVA 577
Db 477 GLTLDTSIIPWASPS-----AGPLPASRCSEPCLONEVKSVQPGEVCCWLCIPQC 526
QY 578 LYPATDLDLDFRCPRCPVKWH-----SGQVPIAKRVFKLVA-TIAPLAFYTIATLSVG 632
Db 527 PYEYRLD--EFTCADCGLYGPNASLTGCFELPOEYIRWGDAMAVGPV---TIACLG--- 578
QY 633 IALAITF-LAFNLHFRKKAIKLSSPKLSNITAVGICFYATVILGLDHSSTLPSAEDSF 691
Db 579 -ALATFLVGLVFRVHNATPVVKASGRELCYLLGGVFLCYCMTFIFAKPST----- 629
QY 692 ATVCTARVYLLSAGFSLAFSGMFATYRVHRIF--TRTGSVFKDKMLQDIDQILVGLGL 749
Db 630 -AVTLRLRLGLGTAFSVCSYALLTKTNRIARIFGGAREGAQ-RPRFISPASQVAICLALI 687
QY 750 LVDALLVTLVWVTDPMERHLNLTLEISATDRSVV-YQPOQVEVCRSHTQTLVSLVYAYK 808
Db 688 SGOLLIVVAWLV-----VEAPGTGKETAPERREYVTLRCHRDASMLGSLAYN 735
QY 809 GLLLVGVYMAWETRHVKIPA-LNDSOYIGVSYSVVTSAIVVLANLISERVTLAFIT 867
Db 736 VLIATLCTLYAFKTR--KCPENFNEARFIFTTITTCI-----IWLAFLP 778
QY 868 ITALILFTST-----TATLCL-----LFIPKLHDI 891
Db 779 I--FYVTSSDYRVQTTTMCVSVLSGSLGVLCGLFAPKLHII 817
RESULT 11
Q62916 PRELIMINARY; PRT; 983 AA.
AC Q62916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hara P.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U47331; AAA88788.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
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QY 647 -----RKLAIKLSSPKLKNITAVG----- 666
DB 1229 IKDDASGRKVPIMKMAOPFIS-FTPIGPRTPNPKAVSFDPRNSTEVMEKYAGIMALLEKYGD 1287
QY 667 -----CIF-----VYATVIL 676
DB 1288 YGHNPRFGCTANEKFCYPSGECVFLKVNRIIGFKTEPYINSDELKAKIDEVEFTALK 1347
QY 677 LGLDHTSL-----PSAEDSFVAVCVARVYLLSAGFSLA 709
DB 1348 RLLENTTTEBGLNRTWITCRSDKDKNVLIEFHPEPAIRTEYTDIEEKIEYIANEGKKSF 1407
QY 710 FG-----SMFAKYRVH-----RIFTRGVSFKDKMLQDIQLILVGLLLVDA 753
DB 1408 FGPNDVNRIVALKIKNLKANERHINCKIVIQSSHPVCNITMFGVITCLISVILLGIDG 1467
QY 754 LTVT-----LWVTDPMERHLNLTLE--ISATDRSVYQPOVEVCRSQHTQWLSVLYAYK 808
DB 1468 RFVSPEYKPIFDPLQRYLETFPLEDPVSTD-DIKIRPELECHESQNSMWGLVGVFK 1526
QY 809 GLLVVGVYMAWTRHYKIPALNDSQYIGSVYSVWITSADVIVVLANLISERVTLAFITI 868
DB 1527 GLTLVGLFLAYETRSIKVQINDSRVGMISYVNVVLCILITAPVGMVIAQQDASFAFV 1586
QY 869 TALILSTTATCLLPIPKLHDIAWRNDIIDPVHSMG-LKMECNTRFRVVDRELOQR 927
DB 1587 ALAVIFCCFLMULLIFVK-----VIEVIRHPKDKAESKYNPDASISKEDEERYQK 1637
QY 928 VEYONRVYKEIQALDAEIRKL-ERLESG-----LTTTSTTSSSTSLTGT 973
DB 1638 LVTENELQRLITQKEKIRVLRQLRVERGDAGKTELNGATGVASAAVATTSQPASLINS 1697
QY 974 GHLKP-ELTVTSG 986
DB 1698 SAHATPAATLAIQOG 1712

RESULT 8
Q23442 PRELIMINARY; PRT; 402 AA.
AC Q23442;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE COSMID ZK180.
GN ZK180.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprout J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Pauley A., Le T.T.;
RA Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U58748; AAB52965.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00003; 7tm3; 1.
DR PROSITE; PS0225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

Query Match 6.4%; Score 429.5; DB 5; Length 402;
Best Local Similarity 33.9%; Pred. No. 1.3e-23;
Matches 103; Conservative 60; Mismatches 104; Indels 37; Gaps 8;

QY 535 BELQOMGKHLFGLVSGPVSFSGPDRVGTAFQIQIGLLEPVALYYPATDALDFRCPRCR 594
DB 11 KMMEAINSSFOGLTKVKFANNERLGLVDIKOWSDGQYVPFAVYDGADD--EFKIIDST 68
QY 595 PVKHSQGVPIAKRVFKLRVATIAPIAFYTIATLSSVGIALAITFLAFLHFKLKAIKL 654
DB 69 TKGW--SPPLDSTTERREHIS-----SILFLAMSLF-----IKM 102
QY 655 SSPKLSNTAVGICFYATVILLGLDHSHTLPSAEDSFATVCTARVYLLSAGFSLAQSMF 714
DB 103 SSPNLNIIAGSICTFASVIMGLD--TRIVSPDVFWVLCYTKTWTLCIGTSLSGAMF 160
QY 715 AKTYRVHRIFRTGVSFKD-KMLQDIQLILVGLLLVDALLVTLVWVDPMERHLNLT 773
DB 161 SKTWRVHSIFT---NIRMDRKAIDSKFIILGILLIDICILVLTWAFVSFSS---YTVT 214
QY 774 LEISATDRSVYQPOVEVCRSQHTQWLSVLYAYKGLLVGVYMAWTRHYKIPALNDS 833
DB 215 ELPHIPENIVILPEVEKCNSSHSGVFOAVLYAVKGLVLMILGCLFLAWEHRHNVN 274
QY 834 QYIG 837
DB 275 KYIG 278

RESULT 9
O96954 PRELIMINARY; PRT; 528 AA.
AC O96954;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE GABA-LIKE RECEPTOR.
GN MGRL.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_TaxID=6047;
RN [1]
RP SEQUENCE FROM N.A.
RX Perovic S., Prokic I., Krasko A., Mueller I.M., Mueller W.E.G.;
RA "Origin of neuronal receptors in Metazoa: cloning of a metabotropic
RA glutamate/-like receptor from the marine sponge Geodia cydonium.";
RL Cell Tissue Res. 0:0-0(0).
DR EMBL; Y17211; CAA76688.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 528 AA; 58641 MW; 0B99D8357FEAB3B1 CRC64;

Query Match 5.3%; Score 356; DB 5; Length 528;
Best Local Similarity 27.6%; Pred. No. 5.8e-18;
Matches 107; Conservative 77; Mismatches 162; Indels 42; Gaps 12;

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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*;"
RL Science 287:2185-2195(2000).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Rote J., Lewis S.E., Blazej R., Davis T.,
RA Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
RA Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
RA Cealniker S., Rubin G.M.;
RT "An exploration of the sequence of a 2.9-Mb region of the genome of
RT *Drosophila melanogaster*: the Adh region.";
RL Genetics 153:179-219(1999).
[3]
RN SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RA Cealniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA Butenhorff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mayda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Swirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RA EMBL; AE003646; AAF53431.1; -
DR EMBL; AE003411; AAF44910.1; -
RA FlyBase; Fgn0028924; GABA-B-RL
DR InterPro: IPR001828; GABA_receptor.
DR InterPro: IPR000337; GPCR_Mgr
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00287; Na_K_ATPase; 1.
DR PROSITE; PS00259; G_PROTEIN_RECPEP_F3_4; 2.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;
KW Hypothetical protein.

Query Match 7.9%; Score 530; DB 5; Length 1713;
Best Local Similarity 15.9%; Pred. No. 4e-30;
Matches 279; Conservative 194; Mismatches 442; Indels 840; Gaps 39;

Qy	28	WAT--	AAAAWEASAEALQALGHEAIRPG-AASTSTSPSSPPGESASTVTAG-----	77
Db	2	WNTTNTAGSRVSSPEYNAKKTEVLQKEIRVKVKNYAPPSPNTPYDPAQAKGAKKKRLM	61	
Qy	78	----	GTPIPRSDWKY---RTVKRRQRQLNSHNLPGSTNASHAH-HLLNLPPRQYL	129
Db	62	KQLHRPQEQRSGORQKHQRRIKRPRRGSSSKAGNNNNNRNI AFLNGTQKKYC	121	
Qy	130	KVNQVFESERMRGPAENRHKG-----IVLGLFELSTSRGP-----	170	
Db	122	-----	WOEFRTLPKGMRTDEGAGWRDMTSDGAVTFWIFLCLIASHPLOGGVAGRDPD	175

Qy	171	-----GLSELGAATMAVEBHNK--RLLPGYTLELVNTDQCPGVGD	211
Db	176	LHIGGIPPIAGKGWGGQACMAARLALDDVNKQPNLLPGFKLILHNSDSECEPLGAS	235
Qy	213	RFFHAIYTQSTRVMVLLGSACSEVYTESLAKVVPYNNIVQVSGSTSPALSDRRREPPFY	272
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Qy	273	RTVAPDSSHNPARIAFIRKFGWGTVTTFQSENEVHLSLVANNVLTELEAANISCAATITPA	332
Db	293	RTHESATVHNPTRIKLMKKEGNSRVALLOQAEVFIETVEDLENRCHMEAGVELVTRQSF-	351
Qy	333	ATDPKEQLLLLRTRDTRIIGSFQELAPOILCEAYRLRMFGADYAWILHESMGAPWMPD	392
Db	352	LSDDPTDAVRNLRQDARIIVGLFVYVAARRVLCMEYKQQLYGRAHVWF-----IGWYED	406
Qy	393	-----QRTACSNEHLOLAYENLIVVSTHNSIVGNVSVISGLNNHMFNSQLRKQSAQ	443
Db	407	NWYEVNLKABGITCTVEQMRIAAGHLTTEALMWNQNNOTTISGMTAEFRVLVLLY----	463
Qy	444	FHGODFGSGYGPRIASATQSDSRRRRRRVGVGTSGH-----LPPEAISOVAPOTYDA	498
Db	464	-----PLLKFLLOCAFELRRHRLNQALIEBGYDINHRYPEGY-QEAPLAYDA	510
Qy	499	VWATALALRAAEHRRNEBQSKLDGFDYTRSDMAWEFLQOMGKLFHVLGVSVPFSFGP-	557
Db	511	VMSVALAFNKTME--RLTTGCKSLRDFTYDKIEADEIYAAMNSTQFLGVSGVWAFSSQG	568
Qy	558	DRVCTTAFYQIQRGLLEPVALYPATDALDF-----	588
Db	569	DRIALTQIEMIDGKYEKLGYYDTQLDNLWLNATEQWIGGKTKHVTTPEPNKNGNP SKDD	628
Qy	589	-----RCPRCRP-----	595
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Qy	596	-----	595
Db	689	FSKQFQESIGVRANRRNSATKKENEKLLVKTVPGKSLIKESNDENVPSRRTKSPQVK	748
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Db	749	KVYEESSTRVREPFDSDFREKLYLSDMIDYDRSSEDVPEKKLSWEPDSTLRRRFSVNNEY	808
Qy	596	-----	595
Db	809	HSSLEGEEEDLDSVGSSTWRGSRYPQNAEDERPVLAEIINMGKLEKELKEQRESTNV	868
Qy	596	-----	595
Db	869	FRNNRRDOKTIDEVKGSKITGTSKQHVVEVKYNETASNEDDDDNAQVKHIGTITTKIFSIAQ	928
Qy	596	-----	595
Db	929	RMKEKKSKESEEDENKDNKVDKENDKODEQKLPPEPEIELEAKKAWTFTPAETSPDI	988
Qy	596	-----VKWHSG-----	601
Db	989	PGENOILQEQYQVKWIGRNRKRYCIGINTDISRKSITKTFFISAGDDLVVYHGGRLKD	1048
Qy	602	-----QVPI-----AKRVEKRLVATIAPLAFYT	624
Db	1049	IGQTTENLNQRKNKHKTTPDDIPVDIGHDDRVEIGVNTKPKLIIPPTAEHMHVK	1108
Qy	625	IATLSSVG-----	632
Db	1109	NGKLRDICTSTDKPFWPIDGDTDVIYMHPIKTRDKKLNLKLVDPDPDNGPYKMPTKEDRR	1168
Qy	633	-----TALAITFLAFLNLFH-----	646
Db	1169	TYKGCYEHFPGRTEWRRLFFNKIHGYKLRPRSHWLYTLVFSVLVILFVIFSMWAFD	1228

QY 181 AVCHINKRLLPGYTLLELVNTDTCDPGVGVDRFEFHAIYTOPSTRMVMMLGSAACEVSTES 240
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QY 241 LAKVVPWNIVQVSFGSTSPALSDRRFPFYRTVAPDSSHNPARIAFIRKFGMGTVTTF 300
DB 241 LAKVVPWNIVQVSFGSTSPALSDRRFPFYRTVAPDSSHNPARIAFIRKFGMGTVTTF 300
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DB 361 PQILCEAYRLRMFGADYAVIILHESMGAPWPDQRTACSNHELQLAVENTLIVVSTHNSLVG 420
QY 421 NNYSYGLNNHMFNSQLRKQSAQFHGQDGFSGYGPRIISAATQSDSRRRRRRGVVGTS 480
DB 421 NNYSYGLNNHMFNSQLRKQSAQFHGQDGFSGYGPRIISAATQSDSRRRRRRGVVGTS 480
QY 481 GHLPFAISQYAPQTYDAVVAIALALRAAEHWRNRNEEQSKLDGFDYTRSDMAWEFLQOM 540
DB 481 GHLPFAISQYAPQTYDAVVAIALALRAAEHWRNRNEEQSKLDGFDYTRSDMAWEFLQOM 540
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DB 781 RSVVYQPOVEVCSQHTQWLSVLYAYKGLLLVGVYMAWETRVKIPALNDSQYIGVS 840
QY 841 YSVVITSAIIVVLANLISERVTLAFITITLITSTTATLCLLFPKLHDIWARNDIIDP 900
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QY 901 VIHSMGLKMCNTRRFVDDRELOQYRVQNRVYKKEIQALDAEIRKLERLLESGLT 960
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DB 1021 SWPSAEMQIPMRSSVTFASQPOLEEAACLPQAQDLINLRLAQQAQTEAKTGILNRLGIFS 1080
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DB 1081 RTTSSNKGSTASLADOKGLKAAFKSHMGLFTRLIPTSSQTSACNAIYNNPNODSIPSEASS 1140
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DB 1201 FOLPNSRRPSVWQPPSLRVRVSGSPRPHRLPPTCSLSALAESEDRPQDSTSIILGSK 1260
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DB 1261 SIPRISLQOVTSGGTWKSMETVCKSRSLSLGDSQEEQQAPANGTE 1305
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Q9VPS7 PRELIMINARY; PRT: 1305 AA.
AC Q9VPS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
CG3022 PROTEIN.
GN GABA-B-R3 OR CG3022
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adam M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwac C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector A., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003588; AAF51465.2; -.
DR FlyBase: FBgn0031275; GABA-B-R3.
DR InterPro: IPR001828; ANF_receptor.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR000005; HTHataC.
DR Pfam: PF00003; 7tm3; 1.
DR Pfam: PF01094; ANF_receptor; 1.
DR PRINTS: PR00248; GPCRMR.
DR PROSITE: PS02529; G_PROTEIN_RECIP.F3.4; 1.
DR PROSITE: PS00041; HTH_ARAC_FAMILY.1; UNKNOWN.1.
DR SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	6705	100.0	1305	5	Q9BML5	Q9bml5 drosophila
2	6671	99.5	1305	5	Q9VP57	Q9vp57 drosophila
3	1229	18.3	1220	5	Q9BML6	Q9bml6 drosophila
4	1228.5	18.3	1221	5	Q9Y133	Q9y133 drosophila
5	1018.5	15.2	840	5	Q9BML7	Q9bml7 drosophila
6	793.5	11.8	816	5	Q9N502	Q9n502 caenorhabdi
7	530	7.9	1713	5	Q9V309	Q9v309 drosophila
8	429.5	6.4	402	5	Q23442	Q23442 caenorhabdi
9	356	5.3	528	5	Q9G954	Q9g954 geodia cydo
10	350.5	5.2	872	4	Q9H3K6	Q9h3k6 homo sapien
11	336	5.0	983	11	Q623916	Q623916 rattus norv
12	329	4.9	879	11	Q9QY52	Q9qys2 mus musculus
13	311.5	4.6	977	13	Q9PWE1	Q9pwe1 ictalurus p
14	307.5	4.6	976	5	Q9V485	Q9v485 drosophila
15	283.5	4.2	1267	5	Q93564	Q93564 caenorhabdi
16	244.5	3.6	940	13	Q73635	Q73635 fugu rubrip
17	244	3.6	1199	11	Q9EPV6	Q9epv6 mus musculus
18	233.5	3.5	1156	13	Q98UC6	Q98uc6 gallus gall
19	233	3.5	856	13	Q73638	Q73638 fugu rubrip

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QY 723 KVRATLRPMKNGRRDSSVCELEQ----RLRDVKNTNCRKALMEKENELQALIRKL- 777
Db 715 rrfqftqndkedsktstsvtnqastrieqlqsenhrimkiteldkleevtmqql 774
QY 778 -GPEARKWIDGVCTCGSNVGSLEPIILNDDIVRLSAPPVRRREMPSTVTMT-SVDSVT 835
Db 775 dtpekttyik-----qnhyqelndiln-----lgnftestdggkail 811
QY 836 STHVEMDNFSVSVQSTVMAPSLPPKKKKSIVESHSHAPATMMQPIQQ-OLQOHLQOQH 894
Db 812 kuhldqn-----pql-----qwnltepsrtckdpiedinspehiqrll 849
QY 895 QMQOQHLOQOQHQQOQQOQQOQQOQHHRHLEKRNVSVA 931
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Search completed: April 30, 2002, 10:00:32
Job time: 575 sec

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Db 655 nvglmciigaavsfldrqpvnqvcivalvifstlclvfpklltltlnpdaatqn 714
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RESULT 15
AAY70326
ID AAY70326 standard; Protein; 898 AA.
AC AAY70326;
XX
DT 21-JUN-2000 (first entry)
DE Human gamma amino butyric acid receptor, GABA-B-R2 protein.
KW Gamma amino butyric acid; GABA-B-R2; human; inhibitory neurotransmitter;
KW central nervous system; anticonvulsant; antispasmodic; antidiarrhetic;
KW uropathic; analgesic; antitussive; agonist; neuroprotective; norepinephrine;
KW treatment; spasticity; incontinence; asthma; drug addiction; nociception;
KW Alzheimer's disease; transgenic animal.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 438..461
FT /label= Transmembrane_domain-I
FT Domain 475..501
FT /label= Transmembrane_domain-II
FT Domain 513..535
FT /label= Transmembrane_domain-III
FT Domain 554..576
FT /label= Transmembrane_domain-IV
FT Domain 612..634
FT /label= Transmembrane_domain-V
FT Domain 648..670
FT /label= Transmembrane_domain-VI
FT Domain 676..701
FT /label= Transmembrane_domain-VII
XX
PN W0200012692-A1.
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XX 09-MAR-2000.
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XX 27-AUG-1999; 99WO-US19651.
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XX 27-AUG-1998; 98US-0141760.
XX 16-OCT-1998; 98WO-US22033.
XX 04-NOV-1998; 98US-0186664.
XX 15-DEC-1998; 98US-0211755.
XX
XX (SYNA-) SYNAPTIC PHARM CORP.
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XX Jones KA, Laz TM, Borowsky B;
PI
XX
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DR WPI: 2000-246751/21.
XX N-PSDB; AA251399.
PT Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for
PT detecting receptor agonists useful for treating e.g. asthma,
PT incontinence, and Alzheimer's disease -
XX
XX Claim 9; Fig 5; 260pp; English.
XX
XX The present amino acid sequence is the human GABA (gamma amino butyric
XX acid)-B-R2 receptor protein isolated from human hippocampus cDNA library.
XX The coding region of GABA-B-R2 is cloned into the expression vector
XX pEX.HRT3T7 and the plasmid is designated as TL-267 (ATCC No. 203515).
XX GABA-B is a major inhibitory neurotransmitter, the receptors of which
XX are widely distributed throughout the central nervous system. GABA-B-R2
XX receptor has anticonvulsant, antispasmodic, uropathic, analgesic,
XX antitussive, antiaddictive, norepinephrine and neuroprotective activity.
XX GABA-B-R2 receptor agonists may be used to treat spasticity, asthma,
XX incontinence, drug addiction, Alzheimer's disease, decrease nociception
XX and as an antitussive agent. Transgenic animals with altered GABA-B-R2
XX levels may be used to determine the physiological effects of varying
XX levels of GABA-B-R2 receptor activity.
XX
XX Sequence 898 AA;
XX
XX Query Match 24.8%; Score 1590; DB 21; Length 898;
XX Best Local Similarity 37.5%; Pred. No. 4.3e-121;
XX Matches 351; Conservative 166; Mismatches 324; Indels 96; Gaps 19;
QY 21 ACGRATKRSVDYIAGFFPYGDGVNSYTGSGVMPKVKALGALGHVNEHGIKILANLYRLHMMWN 80
Db 3 sparsatgplslmgplmctekvakgsigrgvlpavelaieqrne-sllrpyfldrlrly 61
QY 81 DTQCNAAVGVKSFDDMMHSGPNKVMFLFGAACTHTVTDPIAKSKHWHHTQLSYADTHPMFT 140
Db 62 dtecdnakglkatydaikypghlmvggvcpsvtsiaeslgqnlvqisfaattplva 121
QY 141 -KDAFFNFRFVPSNAFNAAPRLALLKEFNWTRGVTVQNEPRYSLPHNHMADLDAMEV 199
Db 122 dkkkpyffrtvpsdnavnpaillkllkhyqkrvgtltdqgvrsevrnditgylgedi 181
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QY 316 LR-GTEYSRPHGYTDGIMAAALAIQV----AEKREDLLTHFDYRVKDWESVFEALR 369
Db 302 krsfgvsgkfhgyaydgviawiaktlgrametlhassrhqrlqdfnfydhtlgrilnamn 361
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Db 421 pkdktiileqlrkisplysilsaltsilnmasafiffnklnrnqklmsspyymnli 480
QY 490 IVGCMITYSIIIFGLDITLSSVAAPFYICTARAWILMAGFSLSFAGFSTWVHIFT 549
Db 481 ilggmsiyasiflfgldgsfvsektfctrtvrtwiltvgytafamaikwrvhaifk 540
QY 550 DLKLNKKVYKDYOLFVWVGVLAIADIAITWQIADPFYR--ETKQLEPLHNEID---- 603
Db 541 nvkmkklkldkqlvlvvggmllidcllcwqavdlrrtveksmep-----dpgar 594
QY 604 DVLVIPENEYCSQSEHMTIFVSIYAYKGLLLVFGAFLAWETRHVSIPALNDSKHGFSVY 663
Db 595 disirpllehcnchtmiwlgivaygylmlfgclawetrnvsipalndskiygmsv 654
```


QY 289 DLLPLSTSGDITVAGITADEYLVEYDLRL-GTEYSRFGHYTDGIIWAALAIQYV----- 342
 Db 318 dfepLsskqiktsgktpqgqyereynnkrsrgvpskfhgdaydgiwvialktlqrametlh 377
 QY 343 AEKREDLLTHFDYRVKDWESVFLALRNTSEGVTPGVRFYNNERNKANILNQFOLGOME 402
 Db 378 assrhqriqdfnydhtlgrilnametnffvgvqvfngermgtikftqfqsrev 437
 QY 403 KIGYHSHQSHLDLSLGKPVKWKGTTPKDRTLIYIEHSQVNPITYIVSASASVIGVIA 462
 Db 438 kvgeynavadtlei-indtirfggseppkdtiileqirkisplysilsaltlilmima 496
 QY 463 TVFLAFNIKRYRNQRYIKMSSPHLNNLIIVGCMITYLSIFLGLDITLSSVAAPFYICTAR 522
 Db 497 safifnknrqnklikmsspymlnllilgmsyasilfgldgsfvsektfetlctvr 556
 QY 523 AWILMAGFSLSFGAMFKSTWVHSIFETDLKLNKKVKIDYQLFMVVGVLDAIDIAITWQ 582
 Db 557 twiltvyttafngamfaktwrvhaifknvnmkikiikdqkllvivggmllldlcilicwq 616
 QY 583 IADPFYR--ETKOLEPLHHEID----DVLVIPENEYQCSEHMTIFVSIYAYKGLLIVF 636
 Db 617 avdplrtvekysemep-----dpagrdisirpllehcenhtmtiwlglivaykgllmif 670
 QY 637 GAFIAWETRVHSIPALNDSKHIGFSVNVFITCLAGAAISLVSLDRKDLVFLVLLFFIIF 696
 Db 671 gcfawetrnvspalndskyigmsvnyvngmciiigaavsfldrqpvnqfivalviif 730
 QY 697 CTATLCLVFPKLVKELKRNQGVV-DKRVRLRPMKNGRRDSSVCELEQ----RLRD 751
 Db 731 csttliclvfpkkitrnpdaatqnrfqtkkedsktsctsvtsvndqastsrleg 790
 QY 752 VKNTNCRFKALMEKENELOALIRKL--GPEARWIDGVTCTGGSVNGSELEPIILNDDIV 809
 Db 791 lqsenhrlmrkiteldkleevtmgldtpekttyik-----qhyqelndlin---- 839
 QY 810 RLSAPPVREMPSTVTVMET--SVDSVSTHVMEDNSFVSQVSTVMAPSLPPKKKQOSIVE 868
 Db 840 -----lgnftestdggkailknhdqn-----pqI-----q 865
 QY 869 HHSHPAPTMQPIQO-QLOQHLOQHOOQOQHLOOQOHOQOQOQOQHHRLEKRN 927
 Db 866 wnttepsrtckpiedinspenhigrisliqpil-----hhaylpsig 908
 QY 928 SVSA 931
 Db 909 gvda 912
 RESULT 13
 AAY44345
 ID AAY44345 standard; Protein; 965 AA.
 XX
 AC AAY44345;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Protein-2 related to human gb2 GABA B receptor.
 XX
 KW gb2 GABA B receptor; human gb2; Hgb2; calcium-sensing receptor;
 KW gamma-amino butyric acid; 4-amino butanoic acid; GABA;
 KW metabotropic glutamate receptor; neurological disorder;
 KW psychiatric disorder; agonist; antagonist.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 100
 FT /note= "encoded by GACCTG"
 XX
 FT
 XX WO9961606-A1.
 XX
 PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11869.
 XX 29-MAY-1998; 98US-0087274.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Clark J, Bonner TI;
 XX WPI; 2000-105616/09.
 DR N-PSDB; AAZ29447.
 XX New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor,
 PT useful for identification of (ant)agonists and for treatment of
 PT neurological disorders -
 XX Disclosure; Page 60-62; 67pp; English.
 XX The present sequence is a protein related to human gb2 GABA B receptor.
 CC Human gb2 (Hgb2) shares sequence homology with rat GABA B receptor rgbl,
 CC parathyroid cell calcium-sensing receptor and metabotropic glutamate
 CC receptors. It can be produced in host cells by transforming them with
 CC recombinant expression vector comprising hgb2 encoding cDNA. The cells
 CC that express the receptor are used in the development of drugs for
 CC treatment of neurological and psychiatric disorders, for pharmacological,
 CC physiological, functional, or other investigational analysis of gb2
 CC GABA B receptor, its agonists or antagonists and for determining the
 CC ability of a chemical to bind to a mammalian gb2 GABA B receptor in
 CC vitro. They may also be used for the preparation of antibodies to hgb2
 CC which can be used in diagnostic assays.
 CC Note: there is no relevant information given about this sequence in the
 CC specification.
 XX Sequence 965 AA;
 SQ
 Query Match 24.8%; Score 1591.5; DB 21; Length 965;
 Best Local Similarity 37.3%; Pred.No. 3.6e-121;
 Matches 360; Conservative 165; Mismatches 328; Indels 111; Gaps 22;
 QY 8 PFASLLFLLL-----WSTACGRTAKRS-DVYIAGFPYGDGVNSYTGKVM 53
 Db 19 pparllllllllppllapgawgawgarprrppssplsimgimpltkevaksgirgv 78
 QY 54 PSVKLAGLVHNEHGKILANVRLHWNNDTCNAAVGVKSFDDMMHSGPNKVMFLFGAACH 113
 Db 79 pavelaieqirne-silrpyfldrly-dtecdnakgikafydaikygnhlmvfvgvcp 136
 QY 114 VTDPIAKAKSHWHLTQLSYADTHPMFT-KDAFPNFRVPVSENAFNAPLALLKEFNWTR 172
 Db 137 vtsiaeslqgnlvqlsfaattpvladkkkypffvtvpsdnavnpaillklkhyqwr 196
 QY 173 VGVYQNEPRYSLPHNHMVDLDAMEVEVETQSFVNDVAESLKKREKDVRIILGNFE 232
 Db 197 vgtltqdvgrfsevrndltgvlgedieidsfdesfndpctsvkklkgndvriilgqfd 256
 QY 233 HFARKAFCEAYKLDVGRAYOWLIMATYSTDW---NVTQDSCESEETATALEGAILV 288
 Db 257 nmaakfvccayeenmygskqwiipgwyepsweweqvteanssrlrnlkaamegyiv 316
 QY 289 DLLPLSTSGDITVAGITADEYLVEYDLRL-GTEYSRFGHYTDGIIWAALAIQYV----- 342
 Db 317 dfepLsskqiktsgktpqgqyereynnkrsrgvpskfhgdaydgiwvialktlqrametlh 376
 QY 343 AEKREDLLTHFDYRVKDWESVFLALRNTSEGVTPGVRFYNNERNKANILNQFOLGOME 402
 Db 377 assrhqriqdfnydhtlgrilnametnffvgvqvfngermgtikftqfqsrev 436
 QY 403 KIGYHSHQSHLDLSLGKPVKWKGTTPKDRTLIYIEHSQVNPITYIVSASASVIGVIA 462
 Db 437 kvgeynavadtlei-indtirfggseppkdtiileqirkisplysilsaltlilmima 495
 QY 463 TVFLAFNIKRYRNQRYIKMSSPHLNNLIIVGCMITYLSIFLGLDITLSSVAAPFYICTAR 522

RESULT 11	
AAAY44344	
ID	AAAY44344 standard; Protein; 914 AA.
XX	AC
XX	AAAY44344;
AC	
XX	
XX	14-MAR-2000 (first entry)
XX	
DE	Protein-1 related to human gb2 GABA B receptor.
XX	
KW	gb2 GABA B receptor; human gb2; Hgb2; calcium-sensing receptor;
KW	gamma-amino butyric acid; 4-amino butanoic acid; GABA;
KW	metabotropic glutamate receptor; neurological disorder;
KW	psychiatric disorder; agonist; antagonist.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	Misc-difference 100
FT	/note= "encoded by GACCTG"
XX	
XX	WO9961606-A1.
XX	
PD	02-DEC-1999.
XX	
XX	28-MAY-1999; 99WO-US11869.
PF	
XX	
XX	29-MAY-1998; 98US-0087274.
PR	
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
PI	Clark J, Bonner TI;
XX	
DR	WPI; 2000-105616/09.
DR	N-PSDB; AAZ29446.
XX	
PT	New GABAB (C-aminobutyric acid or 4-aminobutanoic acid) receptor,
PT	useful for identification of (ant)agonists and for treatment of
PT	neurological disorders
XX	
PS	Disclosure; Page 58-60; 67pp; English.
XX	
CC	The present sequence is a protein related to human gb2 GABA B receptor.
CC	Human gb2 (Hgb2) shares sequence homology with rat GABA B receptor rgbl,
CC	parathyroid cell calcium-sensing receptor and metabotropic glutamate
CC	receptors. It can be produced in host cells by transforming them with
CC	recombinant expression vector comprising hgb2 encoding cDNA. The cells
CC	that express the receptor are used in the development of drugs for
CC	treatment of neurological and psychiatric disorders, for pharmacological,
CC	physiological, functional, or other investigational analysis of gb2
CC	GABA B receptor, its agonists or antagonists and for determining the
CC	ability of a chemical to bind to a mammalian gb2 GABA B receptor in
CC	vitro. They may also be used for the preparation of antibodies to hgb2
CC	which can be used in diagnostic assays.
CC	Note: There is no relevant information given about this sequence in the
CC	specification.
XX	
SQ	Sequence 914 AA;
	Query Match 24.9%; Score 1596.5; DB 21; Length 914;
	Best Local Similarity 37.6%; Pred. No. 1.3e-121;
	Matches 359; Conservative 165; Mismatches 321; Indels 111; Gaps 221
Qy	8 PFASLFLLL-----WSTACGTAKRS-DVYIAGFFPYGDGVENSYTGKVM 53
Db	19 pparllllllllp1lplapagwagwargppppspisimlplmkvaksigrv1 78
Qy	54 PSVKALGHVNEHGKILANYRLHMMWNTQCNAAVGVKSFDDMHSGPNKVMFLFGAACHTH 113
Db	79 pavelaieqrine-sllrpyfidrliv-dtecdnakalkafvdaiakvpnhlmvfgvcps 136

XX	Sequence	941 AA;
Qy	Query Match	24.9%; Score 1598; DB 22; Length 941;
Qy	Best Local Similarity	37.3%; Pred. No. 1e-121;
Qy	Matches 360; Conservative	165; Mismatches 329; Indels 110; Gaps
Qy	8 PFASLLFLL-----WSTACGRTAKRS-DVYIAGFPFYGDGVSNSYTGGRVGM	53
Db	19 pparlllllllpllllapagwargaprpssppplsimglmpitkevaksigrvli	78
Qy	54 PSVKALAGHVNHEGKILANYLRHLMWNDTCNAAVGVKSFEDMMHGPNKVMFLFGAACTH	113
Db	79 pavelateqirne-sllirpyfldrlrydtecdnagkikafydaikygnphmlhfvfgvcp	137
Qy	114 VTDPIAKSKHHHLTQLSYADTHPMFT-KDAFNFPRVVPSENAFNAPRLALLKEFNWTR	172
Db	138 vtsiaeslgdwnlvqisfaatpvladkkkyfirtvpsdnavnpailliklhkqwr	197
Qy	173 VGTVQVNEPRYSLPHNHVADLDLAMEVEVETQSFQNDVAESLKLKEKDVRIILGNFNE	232
Db	198 vgtltqdvqrfsevrndltgvlygedieisdtesfnodpctsvkklkgndvrilqgfdq	257
Qy	233 HFAKAFCEAYKLDWYGRAYQWLIMAYSTDWV-----NVTQDSECVSEIATALEGAILV	288
Db	258 nmaakvfccayeenmygskqwiilpgwyepsweweqvhteanssrcirknllaamegyivg	317
Qy	289 DLLPLSTSGDITVAGITADEVLVEYDRLR-GTEYSRHFHGYTYDGIWAAALAIQYV----	342
Db	318 dfeplsskqiktisgkcpqqyereynnrkgvgspskfhgyaydgviwaktlgramethl	377
Qy	343 AEKREDLLTHFDYRVKDWESVFLEALRNTFEGVTGPVRFYNNERRKANILINOFQLGOME	402
Db	378 assrhqriqdfnytdhlgriilnammetaffgvtggyvfringermgtikftqgdsrev	437
Qy	403 KIGBYHSQKSHLDLSLQKPKVWVGKTPPKDRTLIYIEHSQVNPITYIVSASASVIGVIA	462
Db	438 kvgeynavadtlei-indtrifggseppkdtiileqrlkisiplysailsaltlimgima	496
Qy	463 TVFLAFNIKRYNRQYIKWSSPHLNNLIIVGCMITYILSIIFGLDITLSSVAAFPYICTAR	522
Db	497 safilfnknrqkllkmspsymnnlililgmslgsyasilfgidgsfvsektfctictvr	556
Qy	523 AWILMAGFSLSFAGAMFSKTRWRVHSIFDILKNKVIKDYOLFVMVGVLLAIDAIITWTQ	582
Db	557 twiltvgyttafgamfaktvrvhaifknvkmkklkdkqllvivgmgllidclilicwq	616
Qy	583 IADPFYR--ETKOLEPLJHENID----DVLVIPENECYQSEHMTIFVSIYAYKGLLVF	636
Db	617 avdprrtvekysnep-----dpagrdisirpillehcenthmtiwigivyaykgllmlf	670
Qy	637 GAFIAWETRHVSIPALNDSKHIGFSYVNVITCLAGAAISLVLSDRKDLVFLVLSFFIIF	696
Db	671 gcfawetrnvspalndskvymvnyvgimglgaavsfllrdqpnvqfcivalviif	730
Qy	697 CTTATCLVFPVKLVKLKRNPGQVV-DKRVYRATLRPMKNGRRDSSVCELEQ-----RLRD	751
Db	731 csttilclvfpkllitrtupdtaatqurrffqfqnqkdedsktstsvtnvngastsrleg	790
Qy	752 VKNTNCRFRKALMEKENELQALIRKL--GPEARKWIDGVGTCTGGSNVGSLEPILNDIV	809
Db	791 lqsenhrllmkitelkdleevtmqldtpekttyik-----qnhqyelndiln----	839
Qy	810 RLSAPPVRRMPSTTVTEMT-SVDSVTSTVTHVMDNSFVSVQSVTMVAPSLPPKKKOSIVE	868
Db	840 -----lgnftestdggkaiknlhdqn-----pql-----q	865
Qy	869 HHSHAPAPTMQPIQO-QLQOHLQOHOQMOQOHLQOQOHOQMOQOQOQHHRHLEKRN	927
Db	866 wntteprctkdplredinspehigrllslqpl-----hhaylpsig	908
Qy	928 SVSA	931

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Clark J, Bonner TI;
XX WPI: 2000-105616/09.
DR N-PSDB; AAZ29422.
XX New GABAB (c-aminobutyric acid or 4-aminobutanoic acid) receptor,
PT useful for identification of (ant)agonists and for treatment of
PT neurological disorders
XX Claim 9; Page 26-28; 67pp; English.
XX The present sequence is human gb2 GABA B receptor subunit. Human gb2
CC (Hgb2) shares sequence homology with rat GABA B receptor rgbl,
CC parathyroid cell calcium-sensing receptor and metabotropic glutamate
CC receptors. It can be produced in host cells by transforming them with
CC recombinant expression vector comprising hgb2 encoding cDNA. The cells
CC that express the receptor are used in the development of drugs for
CC treatment of neurological and psychiatric disorders, for pharmacological,
CC physiological, functional, or other investigational analysis of
CC gb2 GABA B receptor, its agonists or antagonists and for determining the
CC ability of a chemical to bind to a mammalian gb2 GABA B receptor in
CC vitro. They may also be used for the preparation of antibodies to hgb2
XX which can be used in diagnostic assays.
XX Sequence 941 AA;

Query Match 24.98; Score 1598; DB 21; Length 941;
Best Local Similarity 37.3%; Pred. No. 1e-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;
QY 8 PFASLLELL-----NSTACGRRTAKRS-DVYIAGFFYPYDGVNSYTCRGVM 53
DB 19 pparlllllllpllapagawargarppppspplslimglptkevakgsigrvll 78
QY 54 PSVKLALGHVNEHGKILANYRLHWMNDTCNAAYGVKSFFDMHSGPNKVMFLPGAACH 113
DB 79 pavelateirne-sllrpyfildrlydtecdnaglkafydaikygnphlmvfgvcps 137
QY 114 VTDPKAKSHWHUQTQSYADTHPMFT-KDAPNPNFRVVPSENAPNAPRALLKEFNWTR 172
DB 138 vtsilaeslgwnlvqisfaattpladkkykpyffrtvpsnavnpaillkikhqyqr 197
QY 173 VGTYYQNEPRYSLBNHNVADLDAMEVEVETQSPVNDVAESLKLREKDVRIILGNFNE 232
DB 198 vgtltqdvqrsevrndltgvlgedieistsesndpctsvkklkgndvriilgqfdq 257
QY 233 HFARKAFCEAYKLDWYGRAYOWLTMATYSTDW-----NVTQDECSVEEITALEGAILV 288
DB 258 nmaakvfccayeemyskyqwiipgwypeswveqvhceanssrclrnllaamegyigv 317
QY 289 DLLPLSTGDTITAGITADEYLVEYDLRL-GTEYSRFGHTYTDGIWAALAIQYV----- 342
DB 318 dfeplsskqiktsgktppqyereynnrsgvpskfgyaydgiwviaktlqrametlh 377
QY 343 AEKREDLLTHFDYRVKDWESVLEALNRTSPEGVTGPRFYNNERKANILINQFOLGOME 402
DB 378 asshrqrldqndhtlgrlilnamnetnfgvtgqvfrngerngmetikftqgdsrev 437
QY 403 KIGBYHQSOKHLDLSLGRPVKVGKTPPKDRTLIIYIEHSONVNTIYIVSASASVIGVITA 462
DB 438 kvgeynavadlel-indtirfgseppkktilleqrkislplylsalsaltllgmlma 496
QY 463 TVFLAFNIKNRYQRIKSSPHNLNLIIVGCMTIIISIFLGLDTLSSVAAPFYICTAR 522
DB 497 saffifnknrqnlkikmssymnnliilgmlsyasiflglqdsfsektfelctvr 556
QY 523 AWILMAFSLSFGAMFSTWRVHSITDOLKLNKKYKIDQYQLFMVGVLLAIDAITTWQ 582
DB 557 twilitvyttafmgafaktwrvaifknvkmkkkikdqkllivvggmllidiclicwq 616

QY 583 IADPFYR--ETKOLEPLHHEID-----DVLVIPENEYCOSEHMTIFVSIYAYKGLLVF 636
DB 617 avdplrttvekysmep-----dpagrdisrlpillecenthmtiwigiyaykglmlf 670
QY 637 GAFLAWETRHSVIPALNDSKHIGFSYVNVITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
DB 671 gclawetrnvsipalndskysgmvyngvimgciigaavsfltrdqpnvqfcivalvif 730
QY 697 CTTATLCLVFPVKLVELKRNPGQVW-DKRVRA TLRPMSKNGRRDSSVCELEQ-----RLRD 751
DB 731 csitilclvfpvklitrltpdaatqnrrfqtgnqkksktsvtsvnqastsrlg 790
QY 752 VKNTRCFRKALMEKENELQALIRKL--GPEARKWIDGVCTGSGNSVNGSELEPILNDDIV 809
DB 791 lqsenhrllmkitelcdkleevlmqldtpekttyk-----qnhyqelndiln---- 839
QY 810 RLSAPPVRREMPSTTVTEMT-SVDSVTSTHVEDMNSFVSOSTVMAPSLPPKKKQSIIVE 868
DB 840 -----lgnftestdggkailknhldqn-----pqj-----q 865
QY 869 HHSAPAPTMQPIQO-QLOOHLOQHOQOQOHLQOQOHOQOQOQOQOHHHLEKRN 927
DB 866 wntepsrtckdledinspehigrslslqpl-----hhaylpsig 908
QY 928 SVSA 931
DB 909 gvda 912
RESULT 9
AAB50088
ID AAB50088 standard; Protein; 941 AA.
XX AAB50088;
XX 19-MAR-2001 (first entry)
DE HG20 protein sequence.
XX Human; HG20; gamma-amino-butyric acid receptor; GABA-B.
XX Homo sapiens.
XX WO200073788-A1.
XX 07-DEC-2000.
XX 30-MAY-2000; 2000WO-CA00638.
XX 01-JUN-1999; 99US-0137025.
XX (MERI) MERCK PROSST CANADA & CO.
XX Ng G, O'Neil G;
XX WPI: 2001-049959/06.
XX N-PSDB; AAC91906.
PT Use of gabapentin, 1-(aminomethyl)cyclohexanecarboxylic acid, in assays for
PT identifying gamma-amino-butyric acid (GABA)-B agonists and antagonists
PT
PS Claim 2; Fig 3; 85pp; English.
XX The present invention relates to a method for determining whether a
CC substance binds to gamma-amino-butyric acid (GABA)-B receptors and is a
CC potential agonist or antagonist of the GABA-B receptor. The method
CC comprises exposing cells to 1-(aminomethyl)cyclohexanecarboxylic acid
CC (gabapentin) in the presence or absence of the substance under
CC investigation. The present sequence is human HG20, which was used in the
CC present invention to construct a functional GABA-B receptor, for use in
CC the method of the present invention.

CC GABAB-R2 as well as a novel, functional GABAB receptor comprising
 CC a heterodimer of GABAB-R1 and GABAB-R2 receptor subunits. It also
 CC relates to variants of the receptors, nucleotide sequences encoding
 CC the receptors, vectors, stable cell lines, antibodies, screening
 CC methods, methods of receptor production, and methods of treatment
 CC or prophylaxis of a disorder that is responsive to modulation of
 CC GABAB receptor activity using a compound that has GABAB receptor
 CC modulating activity. The disorder is especially a CNS disorder, a
 CC gastrointestinal disorder, a lung disorder or a bladder
 CC disorder, especially spasticity, epilepsy, Alzheimer's disease,
 CC pain or an affective or feeding disorder (claimed).
 XX
 SQ Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 21; Length 941;
 Best Local Similarity 37.3%; Pred. No. 1e-121;
 Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLLFLLL-----WSTACGRTAKRS-DVYIAGFFPGDGVNSYTGGRVGM 53
 Db 19 pparlllllllpllapagwargarpppsplimglptkavagsigrv 78
 QY 54 PSVKLALGHVNEHGKILANRYLHMWNNDTCNAAGVKSPFDMHSGPNKVMFLFGAACTH 113
 Db 79 pavelaieqirne-silrpyfldrlydtecdnakgikafydaikygnphlmvfgvcps 137
 QY 114 VTDPTAKASKWHHLTQLSYADTHPMFT-KDAFPNFRVPSENAFNAPRLALLKEFNWTR 172
 Db 138 vtsiaaeslqgnwlvlsfaatpvladkkyppffrtvpsdnvnapailkklkhyqwr 197
 QY 173 VGTVVQNEPRYSPLPHNMVADLDAMEVEVETQSFVNDVAESLKLREKDVRIILGNFNE 232
 Db 198 vgtltqdvrfsevrndltgvlgedieistsfndpctsvkklkgnvriilgfdq 257
 QY 233 HFARAKAFCEAYKIDMYGRAYOWLIMATYSTDWM-----NVTQDSECSVEETATALEGAILV 288
 Db 258 mnaakvfccayeenmygkyqwlipwypsewqevhteanrcrlrknllaamegyigv 317
 QY 289 DLLPLSTSGDITVAGTADLYVEYDLRLR-GTEYSRPHGYTYDGIWAAALAIQYV----- 342
 Db 318 dfeplsskqiktisgktppgyereynkrsgvgsfkfhyaydgviwaktlqrametlh 377
 QY 343 AKREDLLTHFDYRVKDWESVFLEALRNSTFEGVTGPVRYNNERKANILINOLFQOME 402
 Db 378 asshrqiqrqdnfytldtgrliinannetnffgtvgvfrngmrgtkftqfqsrev 437
 QY 403 KIGEYHSQKSHLDLSLGPVKWGPVKPPKPDRTLIYIEHSQVNPITIVSASVIGVIIA 462
 Db 438 kygeynavadtiei-indtirfggseppkdktilleqlrkisiplysisaltilgmlma 496
 QY 463 TVFLAFNIKRYNRQYIKMSSPHLNNLIIVGCMITYLSIIFLGLDTTLSSVAAPFYICTAR 522
 Db 497 saflfnknrqkklmssppmnnliilggmlsyasifligdgsfvsektfctictvr 556
 QY 523 ANILMAGFSLSGAMPKSWRVHSITFDLKLKNKVIKDQOLFVMVGVLLAIDAITTWQ 582
 Db 557 twllvtgyttafamtaktwrhaifknvkmkkkikdkqllvivgmgllidicilicwq 616
 QY 583 IADPFVR--ETQLEPLHENDID---DVLVIPENECQSEHMTIFVSIYAYKGLLLVF 636
 Db 617 avdplrrtvekysmep-----dpagrdlsirpillehcenthmtlwigvyaykgllmlf 670
 QY 637 GAFLAWETHRVSTIPALNDSKHIGFSVYNNVFIITCLAGAAISLVLSDRKDLVFLLSFFIIF 696
 Db 671 gcflawetnrvsipaLndskysgmvyngimcigaavsfldrqpnvqfvaivalvif 730
 QY 697 CTTATLCLVFPKLVKLNKPNQGVW-DKRVRAFLRPMKSNKGRDSSVCELEQ----RLRD 751
 Db 731 cstitclvfpklllrltnpdqaatqnrrfqtqncdkedsktstsvtnqgastsrleg 790
 QY 752 VKNTCNCRFKALMEKENELQALIRKL--GPEARKWIDGVTCCTGGSNVGSLEPIILNDDIV 809

Db 791 lqsenhrlrmkitedldleevtmqlqdtpekttyik-----qnhygelndiln---- 839
 QY 810 RLSAPPVRRPSTTVTEMT-SVDSVTSTHVEDMDSFVSQSTVMAPSLLPPKKKKOSIVE 868
 Db 840 -----lgnftestdgkailknhldqn-----pql-----q 865
 QY 869 HHSAPAPTMQPIQO-QLQOHLQOQMOQOHLQOQOQOQOQOQOQOQOQOQHHRHLEKRN 927
 Db 866 wnttpestrckdpldinspehigrslslqplil-----hhaylpsig 908
 QY 928 SVSA 931
 Db 909 gvda 912
 RESULT 8
 AAY44342
 ID AAY44342 standard; Protein; 941 AA.
 XX
 AC AAY44342;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human gb2 GABA B receptor.
 XX
 KW gb2 GABA B receptor; human gb2; Hgb2; calcium-sensing receptor;
 KW gamma-amino butyric acid; 4-amino butanoic acid; GABA;
 KW metabotropic glutamate receptor; neurological disorder;
 KW psychiatric disorder; agonist; antagonist.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 90
 FT Modified-site 298 /note= "Potential N-linked Glycosylation site"
 FT Modified-site 404 /note= "Potential N-linked Glycosylation site"
 FT Modified-site 453 /note= "Potential N-linked Glycosylation site"
 FT Domain 1..476 /note= "Potential N-linked Glycosylation site"
 FT /label= Amino_terminal_region
 FT /note= "Extracellular"
 FT Domain 477..503
 FT /label= Transmembrane_domain_1
 FT /note= "Hydrophobic and Putative"
 FT Domain 519..543
 FT /label= Transmembrane_domain_2
 FT /note= "Hydrophobic and Putative"
 FT Domain 551..573
 FT /label= Transmembrane_domain_3
 FT /note= "Hydrophobic and Putative"
 FT Domain 594..617
 FT /label= Transmembrane_domain_4
 FT /note= "Hydrophobic and Putative"
 FT Domain 654..675
 FT /label= Transmembrane_domain_5
 FT /note= "Hydrophobic and Putative"
 FT Domain 692..712
 FT /label= Transmembrane_domain_6
 FT /note= "Hydrophobic and Putative"
 FT Domain 718..746
 FT /label= Transmembrane_domain_7
 FT /note= "Hydrophobic and Putative"
 XX
 PN WO9961606-A1.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11869.
 XX
 PR 29-MAY-1998; 98US-0087274.

QY 54 PSVKLALGHVNEHGKILANYRLHMWNNDTCNAAYCVKSFDFDMHSGPNKVMFLGCACTH 113
Db 79 pavelaieqrne-silrpyfldrlrytedcnakglkaifydaikygnphlmvfgvcp 137
QY 114 VTPIAKASHWHLTQLSYADTHPMFT-KDAFPNFRVVPVPSNAFAPRLALLKEFNWTR 172
Db 138 vtsiaeslgqwnlvqisfaattvpvlaadkkyppffrtvpsdnvnpailkilkhyqwr 197
QY 173 VGTYYQNEPRYSPLPHNHVADLDAAVEVEVETQSVNDVAESLKKLRKDKDVRRIILGNFNE 232
Db 198 vgtltqdvrfsevrndltgylgedieidsdesndpctsvkklkgnndvrlilgqfdq 257
QY 233 HFARKACEAYKLDMYGRAYOWLIMATYSTDW-NTQDSECSVEBIATALEGAILV 288
Db 258 nmaakvccayeeemyskywipgwpeweqvhteanssrcrlrknllaamegyigv 317
QY 289 DLLPLSTSGDITVAGITADEVLEVDRLR-GTEYSRFGHYTVDTGIAAALATQYV---- 342
Db 318 dfepsskqiktisgktpqgyereynkrsgvgsfkfgyaydgilwviaktlqrameth 377
QY 343 AEKREDLLTHFDYRVKOWESVLEALRNTSPFVTPGVFRVYNNERKANILINQFOLGOME 402
Db 378 assrhqridfnydhtlgrilnamnetnffvgtgvfrngermgtkikftqfqsdev 437
QY 403 KIGYHSQKSHLDLSLGPVKVWCKTPPKDRTLVIHESQVNPITYIVSASASVIGVITA 462
Db 438 kvgeynavadtlei-indtirfgsepkktilleqirklisplysalsaltlilgmlma 496
QY 463 TVFLAFNKYRNORYIKMSSPHLNLITVGMITVLSIFLGLDITLSSVAAPFVICTAR 522
Db 497 safflfnknrqnklmsspymnllilgmlsyasflfgldgsfsektfetictr 556
QY 523 AWILMAGFSLSFGAMFSKTWVHSIFTDLKLNKKVICKDYQLFMVYVGLIAIDIAITWQ 582
Db 557 twiltvyttafmgafaktwrvaifknvkmkikiqkllivvgmllldlcilicwq 616
QY 583 IADFPYR--ETKQLEPLHENDID----DVLVIPENYCOSEHMTIFVSIYAYKGLLVF 636
Db 617 avdplrtvekysnep-----dpagrdisirpllehcenhtmtlwlgiyaykylmif 670
QY 637 GAFLAWETRHSIPALNDSKHIGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLLFFIIF 696
Db 671 gcfawetrnvspalndskylgmsvnyvngmcilgaavsvfltrdqpnpvqfcivalviif 730
QY 697 CTTATCLLVFPKLVKLEKPGQVY-DKRVRLATLRPMKNGRRDSSVCELEQ-----RLRD 751
Db 731 cstlclvfpkltitrtnpdaatqnrrftqtkkedsktstsvtsvndqastsrleg 790
QY 752 VKNTNCRFKALMEKENELQALIRKL--GPEARKWIDVGTCTGGSNVGSELEPIILNDDIV 809
Db 791 lqsenhrmrkiteldkleevtmqldtpekttyik-----qnhyqelndiIn---- 839
QY 810 RLSAPPVRRMPSTVTEMT-SVDSVSTHVEDMDSFVSQSVTVMAPSLPPKKKQSIVE 868
Db 840 -----lgnftestdggkailknhdqn-----pql-----q 865
QY 869 HHSAPATPMQPIQQ-OLQOHLQOHOQOQOHLQOHOQOQOQOQOQOQOQOQOQOQOQO 927
Db 866 wntteprtckpiedinspehigrilqlpil-----hhaylpsig 908
QY 928 SVSA 931
Db 909 gvda 912

RESULT 7
ID AAY79202
AC AAY79202 standard; Protein; 941 AA.
XX AAY79202;
XX AAY79202;
DT 19-JUN-2000 (first entry)
XX

DE Human GABAB receptor 2.
XX GABAB receptor 2; GABAB-R2; human; bladder disorder;
KW gastrointestinal disorder; central nervous system disease;
KW lung disorder; spasticity; epilepsy; Alzheimer's disease; pain;
KW affective disorder; feeding disorder; diagnosis; therapy;
KW G-protein coupled receptor; GABA; gamma-aminobutyric acid;
KW signal transduction.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..41 /note= "signal peptide"
FT Protein 42..941 /note= "mature protein"
FT Domain 481..504 /note= "transmembrane domain I"
FT Domain 519..544 /note= "transmembrane domain II"
FT Domain 557..578 /note= "transmembrane domain III"
FT Domain 597..618 /note= "transmembrane domain IV"
FT Domain 634..676 /note= "transmembrane domain V"
FT Domain 690..713 /note= "transmembrane domain VI"
FT Domain 719..744 /note= "transmembrane domain VII"
FT Modified-site 90 /note= "N-glycosylated"
FT Modified-site 298 /note= "N-glycosylated"
FT Modified-site 389 /note= "N-glycosylated"
FT Modified-site 404 /note= "N-glycosylated"
FT Modified-site 453 /note= "N-glycosylated"
FT Modified-site 562 /note= "N-glycosylated"
XX WO200014222-A2.
XX 16-MAR-2000.
XX 03-SEP-1999; 99WO-GB02918.
XX 07-SEP-1998; 98GB-0019420.
XX 09-OCT-1998; 98US-0103670.
XX (GLAX) GLAXO GROUP LTD.
XX Barnes AA, Wise A, Marshall FH, Fraser NJ, White JHM, Foord SM;
XX WPI; 2000-256974/22.
XX N-PSDB; AA294168.
XX GABA-B receptor subtypes useful for identifying modulators of GABA-B
XX receptor activity that may be used for preventing and treating diseases
XX including Alzheimer's disease, epilepsy and spasticity -
XX Claim 11; Fig 1B; 67pp; English.
XX The present sequence is that of a novel human GABAB receptor
XX subtype, GABAB-R2, as deduced from a cDNA clone (see AA294168)
XX isolated from human cerebellum cDNA on the basis of homology to
XX rat GABA-R1a and 1b splice variants. GABAB receptors are members
XX of the 7-transmembrane G-protein coupled receptor superfamily.
XX Activation results in signal transduction through a variety of
XX pathways mediated principally via members of the Gi/Go family of
XX pertussis toxin-sensitive G-proteins. GABAB-R2 is specifically
XX expressed at high levels only in the central nervous system (CNS).
XX The invention relates to novel GABAB subtypes GABAB-R1c and

CC sequence represents the human GABA-B receptor described in the method of
CC the invention.

XX Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 21; Length 941;
Best Local Similarity 37.3%; Pred. No. 1e-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLLLELL-----WSTACGRRTAKRS-DVYIAGFFPYGSGVNSYTGRCVM 53
DB 19 pparllllllllppllapagawgargprppspplslmgplmkavksgirgvl 78
QY 54 PSVKLALGHVNEHGKILANRYLHMMWNDTCNAAGVGVKSFDDMMHSGPNKVMKFGAACTH 113
DB 79 pavelaieqrne-sllrlyfildrlrlytedcdnagkafydaikygnhlmvfgvcps 137
QY 114 VTDPIAKASHWHLTQLSYADTHPMFT-KDAFPNFRVPSSENAFNAAPRLALLKEFWNTR 172
DB 138 vtsiaeslqgwlvlsfaatpvladkkkypfyrtpsdnavnpailkllkhyqwr 197
QY 173 VGTVYQNEPRYSLPHNHMVAADLAMEVEVETQSFVNDVAESLKKLEKDVRIILGNFNE 232
DB 198 vgtltdqgrfsevrndltgvlgedieidsfndpsvskkngdvriilgqfdq 257
QY 233 HFARKAFCAEKYKIDMYGRAYQWIMATYSTDW-----NVTQDSECSVEETATALEGAILV 288
DB 258 nmaakvfccayeenmygskylwipgwypswweqvhteansrcrlknllaamegyigv 317
QY 289 DLLPLSTSGDITVAGITADYLYVEYDRLR-GTEYSRPHGYTYDGIWAAALAIQV----- 342
DB 318 dfeplsskqiktisgktpqqrereynkrsgvgpskfhgvydgivwiaktlgrametlh 377
QY 343 AEKRELLTHFDYRVKDWESVFEALRNTSFGVTGVPVRYNNERKANILINQFOLQOME 402
DB 378 asrhrigdqfnytdhtlgrilnmetnffgvtgvqvfngermgtikftqfqsrev 437
QY 403 KIGEYHSQSHLDLSLGPVKVKGKTPPKDRTLIYIEHSQVNFTIYIVSASVIGVIA 462
DB 438 kvgeynavadtlei-indtrifsgseppkdktilleqlrkislpysilsaltlilmima 496
QY 463 TVFLAFNIKRYNORYKMSPHNLNLIIVCCMTYLSIIFGLDITLSSVAAPFYICTAR 522
DB 497 safifnknrdnkllkmspsymnnlilggmsysaiflfgidgsvfsektfcltctr 556
QY 523 AWTLMAGFSLSFGAMPSKTRWRVHSITDLKLNKVIKDYOLFVWGVLLADIAIITWQ 582
DB 557 twiltvgytatagmfaktwrhvaifknvkmkkikdkqlvlivggmllidicilcwq 616
QY 583 IADPFYR--ETKOLEPLHHEID----DVLVIPENECYQSEHMTIFVSIYAYKGLLVF 636
DB 617 avdplrtvekysmep-----dpagrdisrpllethcenthmtiwigvaykglmlf 670
QY 637 GAFLAWETHRVSPALNDSKHIGFSVYNVFTCLAGAAISLVISDRKDLVFLVLSFFIF 696
DB 671 gcflawetrnvspalndskylgmsvynvgimcligaavsflltrdgnvqfcivalvif 730
QY 697 CTTATLCVFPVKELKRNPGQV-DKVRATLRPMKNGRRDSSVCELEQ-----RLRD 751
DB 731 cttatlcivfpvkilrltnpdnatqnrffqftqngkdkststsvtsvngastslreg 790
QY 752 VRNTNCRFRKALMEKENELQALIRKL--GPEARKWIDGVTCGTGGSNVGSELEPLINDDIV 809
DB 791 lqsenhrlrmkiteldkdlleevtmqlgdtpekttyik-----qhnyqelndiln---- 839
QY 810 RLSAPPVRREMPSTVTTEMT-SVDSVTSTHVMENDSNFVSQSVTMVAPSLPKKKQKQSI 868
DB 840 -----lgnftestdggkailknhdqn-----pql-----q 865
QY 869 HHSHPAPTMQPIQ-QLOOHLQHQHQOQOHLQOQOQOQOQOQOQOQOHHHLEKRN 927
DB 866 wntptsrctkdpiedinspehiqrilsilqlpil-----hhaylpsig 908

Oy 928 SVSA 931
DB 909 gvda 912

RESULT 6

AAAY70328
ID AAAY70328 standard; Protein; 941 AA.

XX AAAY70328;

XX 21-JUN-2000 (first entry)

XX Human GABA-B-R2 receptor protein version-1.

XX Gamma amino butyric acid; GABA-B-R2; human; inhibitory neurotransmitter;
XX central nervous system; anticonvulsant; antisthmatic; antiaddictive;
XX uteropathic; analgesic; antitussive; agonist; neuroprotective; nootropic;
XX treatment; spasticity; incontinence; asthma; drug addiction; nociception;
XX Alzheimer's disease; transgenic animal.

XX Homo sapiens.

XX WO200012692-A1.

XX 09-MAR-2000.

XX 27-AUG-1999; 99WO-US19651.

XX 27-AUG-1998; 98US-0141760.

XX 16-OCT-1998; 98WO-US22033.

XX 04-NOV-1998; 98US-0186664.

XX 15-DEC-1998; 98US-0211755.

XX (SYNA-) SYNAPTIC PHARM CORP.

XX Jones KA, Laz TM, Borowsky B;

XX WPI; 2000-246751/21.

XX N-PSDB; AAZ51401.

XX Novel nucleic acids encoding a GABA-B-R2 polypeptide, useful for

XX detecting receptor agonists useful for treating e.g. asthma,

XX incontinence, and Alzheimer's disease.

XX Claim 16; Fig 23; 260pp; English.

XX The present amino acid sequence is the version-1 of human GABA (gamma

XX amino butyric acid)-B-R2 receptor protein, isolated from human

XX hippocampus cDNA library. GABA-B is a major inhibitory neurotransmitter,

XX the receptors of which are widely distributed throughout the central

XX nervous system. GABA-B-R2 receptor has anticonvulsant, antisthmatic,

XX uteropathic, analgesic, antitussive, antiaddictive, nootropic and

XX neuroprotective activity. GABA-B-R2 receptor agonists may be used to treat

XX spasticity, asthma, incontinence, drug addiction, Alzheimer's disease,

XX decrease nociception and as an antitussive agent. Transgenic animals

XX with altered GABA-B-R2 levels may be used to determine the physiological

XX effects of varying levels of GABA-B-R2 receptor activity.

XX Note: This sequence is an alternative version of the human GABA-B-R2

XX receptor protein sequence given in Fig. 5 (AAAY70326).

XX Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 21; Length 941;

Best Local Similarity 37.3%; Pred. No. 1e-121;

Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

Oy 8 PFASLLLELL-----WSTACGRRTAKRS-DVYIAGFFPYGSGVNSYTGRCVM 53

DB 19 pparllllllllppllapagawgargprppspplslmgplmkavksgirgvl 78

CC of (A) with G-proteins or other signal transduction molecules. The
CC analysis of the interactions of (A) and GABA-B receptors is important
CC for identifying potential active substances against diseases such as
CC epilepsy, stroke and psychological diseases such as stress, manic
CC depression, schizophrenia, migraine and others. This sequence represents
CC the human GABA-B receptor described in the invention.
XX

SQ Sequence 941 AA;

Query Match 24 98; Score 1598; DB 21; Length 941;
Best Local Similarity 37.38; Pred. No. 1e-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLFLLL-----WSTAGCRATKRS-DVVIAGFFPYGDCVENSYTCRGVM 53
DB 19 pparlllllllllpllapagwargaprrppssplimglmlptkevagsigrvll 78
QY 54 PSVKALGHVNEHGKILANYRLHMWNDCNAAYGVKSFFDMHSGPNKVMFLFGAACH 113
DB 79 pavelaieqrne-sllrpyfldrllydtecdnakglkafydaikygnphlmvfgvcps 137
QY 114 VTDPPIAKASHWHLTQLSYADTHPMFT-KDAFPNPFRRVVPSENAPRLALLKEFNWTR 172
DB 138 vtsiaeslgwnlvqisfaatpvladkkykyfirtvpsdnavnppaillklkhqykr 197
QY 173 VGTYYQNEPRYSPLPHNMVADLAMEVEVETQSPVNDVAESLKKLREKDVRIILGNPNE 232
DB 198 vgtitqdvrfsevrndltgylgedieisdtcsfnpctsvkllkngndvriilgqfqq 257
QY 233 HFARKAFCEAYKLDYGRAYQWLIMATYSTDMW-----NVTQSECSVEEIIATALEGAILV 288
DB 258 nmaakvfocaeenmygskyyiipgwypswewqvheteansrrclrknlleaamegyigv 317
QY 289 DLLPLSTSGDITFAGITADEYLVEYDLRL-GTEYSRFHGYTYDGIWAALAIQYV----- 342
DB 318 dfeplsskqiktisgktpqgyereynnrsgvgpskfhyaydgviaktlqrametlhr 377
QY 343 AEKREDLLTHFDYRVKDWESFLEALRNTSPGTVRFPYNNERKANLINOFGOLGOME 402
DB 378 assrhqriqdfnydhtlgrilnaamntnffgvtgqvvrngermgtkikftqfqsrev 437
QY 403 KIGYHSQKSLDLSLGRPVWVGKTPPKDRFLIYIEHSQVNPTIYVSASASVIGVITA 462
DB 438 kvgeynavadtclei-indtirfqseppkdktilleqlrkisplysiltsaltlilgmlma 496
QY 463 TVFLAFNIKRYNORYIKMSSPHNLNLIIVGCMITYLSIFLGLDTLSSVAAPFYICTAR 522
DB 497 saffifniknrnqkllkmspymnnlilggmlsyasiflglgsvfsektfetlctvr 556
QY 523 AWILMAGFSLSGAMFSTWRVHSITDILKLNKKVYKIDYOLPMVGVLLAIDIAITTTWQ 582
DB 557 twiltvgytafagmfaktwrvaifknvkmkklkdkqllivivggmllidclilicwq 616
QY 583 IADPFYR--ETKQLEPLHHEID----DVLVITPENYCOSEHMTIFVSIYIYAKGLLLVF 636
DB 617 avdplrtvkeysmep-----dpagrdisirpllehcenhtmtlwlgiyvykylmlif 670
QY 637 GAFLAWETHRHSIPALNDSKHIGFSVYVWFTCLAGAAISVLSDRKDLVFLVLSFFIIP 696
DB 671 gcfawetrnvspalndskylgmsvynvglmciigaavsfldrqpnnvgfcivaliilf 730
QY 697 CTTATLCILVFVKELARNPGQVV-DKRVATRLRPMKNGRRDSSVCELEO-----RLRD 751
DB 731 cstitclilvfvpkklitrlnpdaatqnrfqtnqkksdstsvtsvngastsrleg 790
QY 752 VKNTNCFRKALMEKENELQALIRKL--GPEARKWIDVTCRGGSNVSGSELEPILNDDIV 809
DB 791 lqsenhrllrmkiteldkdeevtmqlqdtpekttyik-----qnhyqelndiln---- 839
QY 810 RLSAPPVREMPSTTVTEMT--SDVSVTSTHVEMDNSFVSQVTWAPSLPPPKKKKOSIVE 868
DB 840 -----lgnftestdgkailknhdqn-----pqI-----q 865

QY 869 HHSHAPAPTMQPIQQ-QLQQHLLQQHQOQQOQHLLQOQQHQOQQOQQOQHHLRLKRN 927
DB 866 wnttepsrtckdpiedinspehigrisllqlpil-----hhaylpsig 908
QY 928 SVSA 931
DB 909 gvda 912

RESULT 5

AY51928

ID AAY51928 standard; Protein; 941 AA.

XX AAY51928;

XX 22-JUN-2000 (first entry)

XX Human GABA-B receptor protein.

XX GABA-B receptor; neuroprotectant; gene therapy; central nervous system;

XX metabotropic receptor; signal transduction; epilepsy; stroke; migraine;

XX psychological disease; stress; manic depression; schizophrenia; human.

XX Homo sapiens.

XX DE19841941-A1.

XX 16-MAR-2000.

XX 14-SEP-1998; 98DE-1041941.

XX 14-SEP-1998; 98DE-1041941.

XX (BADI) BASF-LYNX BIOSCIENCE AG.

XX Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;

XX WPI: 2000-257875/23.

XX N-PSDB; AA289485.

XX A novel metabotropic receptor complex from the central nervous system,

XX related coding sequences and methods of identifying binding substances,

XX ligands and interactions with other proteins

XX Claim 1; Page 26-29; 32pp; German.

XX This invention describes a novel protein heteromer, containing at least
CC a GABA-B receptor protein and at least a protein (A) or its derivative
CC which retains the biological activity of the protein heteromer. The
CC protein of the invention has neuroprotective activity and can be used
CC for gene therapy. (A) or the protein heteromer are useful for identifying
CC proteins (or nucleic acids encoding such proteins) that show specific
CC binding affinity to (A) or the protein heteromer. The two-hybrid system
CC or biochemical methods can be used to identify interaction domains of
CC metabotropic receptors and use for pharmacotherapeutic intervention.
CC Structural information from the protein or protein complex is useful for
CC identifying and manufacture of substances which have specific binding
CC activity to the protein or protein complex. The protein heteromer and (A)
CC or fragments of these are useful as antigens to generate specific mono-
CC or polyclonal antibodies. The encoding nucleic acid (I) is useful for
CC identifying and isolating homologous sequences, as a marker for human
CC disease and for gene therapy. The methods can be used to identify
CC substances, which bind to (A) or (I) and that cause inhibition or
CC activation of functional effects of the GABAergic signal messages in
CC neurons of the central nervous system. The method can also identify
CC substances that inhibit or amplify interactions of (A) with other
CC metabotropic receptors or interaction of ligands with the protein
CC heteromer or (A) or interactions of (A) with G-proteins or other signal
CC transduction molecules. The analysis of the interactions of (A) and
CC GABA-B receptors is important for identifying potential active substances
CC against diseases such as epilepsy, stroke and psychological diseases such
CC as stress, manic depression, schizophrenia, migraine and others. This

CC The present sequence represents a human gamma-amino-butyric acid (GABA)
CC B receptor (GABABR) subunit designated HG20. The present invention
CC also describes the GABABR subunit designated GABABR1A. Cells expressing
CC the new receptor subunits are useful for identifying GABABR agonists
CC and antagonists. HG20 proteins and their antagonists are useful for
CC inhibiting HG20 or GABABR function, useful for treating depression,
CC epilepsy, neuropsychiatric disorders, dementias, muscular contractions,
CC and central nervous system disorders.

XX Sequence 941 AA;

Query Match 24.9%; Score 1598; DB 20; Length 941;
Best Local Similarity 37.3%; Pred. No. 1e-121;
Matches 360; Conservative 165; Mismatches 329; Indels 110; Gaps 21;

QY 8 PFASLLFLLL-----WSTACGRTAKRS-DVYTAGFPFPGDGVNSYTGRCVM 53
DB 19 pparllllllllppllapagawargap:pppsppisimglmlptkevagsigrvli 78
QY 54 PSYKLAGHVNHRGKILANRYLHMWNNDTCNAAVGVKSFDDMMHSGPNKVMFLFGAACH 113
DB 79 pavelaieqrne-silrpyfldrlrydtecdnagkikafydaikypgnhlmvfgvcps 137
QY 114 VTDPIDAKSKWHHLTQLSYADTHPMFT-KDAFPNFFRVVSENAFNAPRLALLKEFNWTR 172
DB 138 vtsiaeslgwnlvqlsfaatpvladkkkypffrtvpsdnavnpaillklkhyqwr 197
QY 173 VGVNYNEPRYSPLPHNMVADLAMEVEVVTOSFVNDVAESLKLREKOVRIITLGNFNE 232
DB 198 vgitqdvrfsevrnditgvlgyedeisdesfsndpctsvkklgndvriilgqfdq 257
QY 233 HFARKAFCEAYKLDYGRAYOWIMATYSTDW-----NVTQDSECSVEETATALEGALLV 288
DB 258 nmaakvfccayeenmgykgywiipgwyepswqeavteansrclrknlilaamegyivg 317
QY 289 DLLPLSTGDIIVAGITADYELVEYDRLR-GTEYSRPHGYTYDGIWAAALAIQV----- 342
DB 318 dfeplsksqiktsgktppqgyreyennkrsgvgpskfhgyaydgivwiaktlgrametlh 377
QY 343 AEKREDLLTHFDYVRDWSVFLEARNSTSEGTGCPVRYNNERKANILINQFOLQOME 402
DB 378 assrhrgidfnvtdhtlgrlllnammetnffvgvgringermgtikftqfdqrev 437
QY 403 KIGEYHSQSHLDSLGKPKPKDRTLIYIEHSGVNPPTIYIVSASVIGVITIA 462
DB 438 kvgeynavadtlei-indtirfgseppkdtilelqrkislplysiltsaltlilmima 496
QY 463 TVFLAPNIKYRNORYIKMSSPHLNLIIVGCMITYLSIIFGLDPTTLSSVAAPFYICTAR 522
DB 497 safflnknrqkllkmsppymnnlilggmlsyasafiflgldgstfvsektfetlctvr 556
QY 523 AWILMAGSLSFCAMPSKTRVHSIFTDLKNKVKIDYOLFVWVGVLDAIDIAIITWQ 582
DB 557 twltyvgytafagmaktwrhaifknvkmkikiidqkllvlgvgnlildcillcawq 616
QY 583 IADPVPFR--ETKOLEPLHHEID----DVLVIPENECQSEHMTIFYSIYAYKGLLVF 636
DB 617 avdplrrtvekysmep-----dpagrdisirpillehcenthtmiwlgvyaykgllmlf 670
QY 637 GAFLAWETHRVSTIPALNDSKHGFSVYNVFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
DB 671 gcfawetnrvsfpalndskysgmvsyngvimglgaavsflltrdqpnvqfcivalvif 730
QY 697 CITATLCLVFPKLVKLPKRNQGVV-DKRVRAILRPMKSKNGRDRSSVCELEQ-----RLRD 751
DB 731 cstltclvfpklltrlnpndaatqnrrftqngkksdsktsstsvtnqatsrleg 790
QY 752 VKNTNCRFKALMEKELQALIRKL--GPEARKWIDGVTCGSSNVGSELEPLTNDIV 809
DB 791 lqsenhrlmkitelkdleevtmqldtpekttylk-----qnhylgelndlin---- 839
QY 810 RLSAPPVRRPMPSTTWTMT--SVDSVSTSTHVMDNSFVSQSTVWAPSLPPKKKKQISIVE 868

DB 840 -----lgftestdgkailknhdqn-----pql-----q 865
QY 869 HHSHAPAPTMPIQQ-QIQQLHQ 927
DB 866 whtpepstckdpiedinspehiqrslslpil-----hhaylpsig 908
QY 928 SVSA 931
DB 909 gvda 912

RESULT 4

AAW90938
ID AAW90938 standard; Protein; 941 AA.

XX AC AAW90938;

XX DT 14-JUL-2000 (first entry)

XX DE Human GABA-B receptor protein.

XX KW GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor;
KW human disease marker; gene therapy; central nervous system; epilepsy;
KW stroke; psychological disease; stress; manic depression; schizophrenia;
KW migraine.

XX OS Homo sapiens.

XX PN WO200015786-A1.

XX PD 23-MAR-2000.

XX PF 11-SEP-1999; 99WO-EP06742.

XX PR 14-SEP-1998; 98DE-1041941.

XX PR 04-DEC-1998; 98DE-1056066.

XX PA (BADI) BASF-LYNX BIOSCIENCE AG.

XX PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;

XX DR WPI; 2000-283281/24.

XX DR N-PSDB; AAA11696.

XX PT A novel metabotropic receptor complex from the central nervous system,
PT related coding sequences and methods of identifying binding substances,
PT ligands and interactions with other proteins

XX PS Claim 5; Page 53-56; 66pp; German.

CC This invention describes a novel protein heteromer, containing at least
CC a GABA-B receptor protein and at least a protein (A) or a sequence which
CC has a substitution, inversion, insertion or deletion of one or more amino
CC acid residues and which retains the biological activity of the protein
CC heteromer and which has neuroprotective activity. The encoding nucleic
CC acid (I), the construct, (A) or the protein heteromer are useful for
CC identifying proteins (or nucleic acids encoding such proteins) that show
CC specific binding affinity to (A) or the protein heteromer. The two-hybrid
CC system or biochemical methods can be used to identify interaction domains
CC of metabotropic receptors and use for pharmacotherapeutic intervention.
CC Structural information from the protein or protein complex is useful for
CC identifying and manufacture of substances which have specific binding
CC activity to the protein or protein complex. The protein heteromer and
CC (A), or fragments of these are useful as antigens to generate specific
CC mono- or polyclonal antibodies. (I) is useful for identifying and
CC isolating homologous sequences, as a marker for human disease and for
CC gene therapy. The methods can be used to identify substances, which bind
CC to (A) or (I) and that cause inhibition or activation of functional
CC effects of the GABAergic signal messages in neurons of the central
CC nervous system. The method can also identify substances that inhibit or
CC amplify interactions of (A) with other metabotropic receptors or
CC interaction of ligands with the protein heteromer or (A) or interactions

XX PR 03-APR-1998; 98US-0080676.
 XX PA (NPSP-) NPS PHARM INC.
 XX PI Garrett JE, Simin RT, Busby JG, Stormann TM;
 XX WI WPI; 1999-610994/52.
 DR N-PSDB; AAX90919.
 XX Novel nucleic acids, used to screen for specific modulators, e.g. for
 PT treating spasticity or Alzheimer's disease
 PT Claim 5; Fig 2A-2F; 78pp; English.
 XX The present sequence is the human GABABR2 receptor protein. GABAB
 CC receptors are metabotropic receptors that modulate synaptic transmission
 CC in brain. GABABR2 is closely related to GABABR1 and GABABR3. GABABR2
 CC polypeptides are produced using recombinant nucleic acid techniques. They
 CC are used to raise antibodies and to identify specific modulators of
 CC GABABR2. These modulators are useful for treating spasticity, motor
 CC control disorders etc. The antibodies are used as therapeutic modulators,
 CC for GABABR2 quantification, affinity purification and to study synthesis,
 CC structure and function of the receptor.
 XX SQ Sequence 943 AA;

Query Match 25.08; Score 1602; DB 20; Length 943;
 Best Local Similarity 35.78; Pred. No. 4.8e-122;
 Matches 369; Conservative 172; Mismatches 344; Indels 148; Gaps 23;

QY 8 PFASLLFILL-----WSTAGRTAKRS-DVVIAGFFPYGCGVENSYTGGRVM 53
 Db 19 pparlllllllllplapagawgargarpppsppisimglmlptkevagsigrvl 78
 QY 54 PSVKALGHVNEHGKILANYRLHMMWNTQCNAAVGVKSFEDMHSGPNKVMFLGAACPTH 113
 Db 79 pavelaieqrne-sllrpyfidlrlytecdnaklkafydaikygnhlmvfgvcps 137
 QY 114 VTDPAAKSKHWHLTOLSYADTHPMFT-KDAFPNFRVVPSENAPNAPLALLKEFNWTR 172
 Db 138 vtsiaeslqgnvlvqlsaattppvladkkyppfrtvpssnavnpaalkkilykqwr 197
 QY 173 VGTYYQNEPRYSLPHNHMVADLDAMEVWETQSVNDVAESLKLREKDVRIILGNFNE 232
 Db 198 vgtltqdvqrfservndltgylgedicisdesfndpctsvkklkndvriilgqfqq 257
 QY 233 HFARAFCEAYKLDYGRAYQWLIMATYSTDW-----NVTDSECSVEEIIATALEGAILV 288
 Db 258 nmaakvfccayeenmygskypqilpgwyepswqevhteanssrcrlrknllaamegyigv 317
 QY 289 DLLPLSTSGDITVAGITADEYLVEYDRLR-GTEYSRFHGYTYDGIWAALAIQYV----- 342
 Db 318 dfeplsskqiktisgktppqyereynnrsvgvpkskfghyaydgiwviaktlqrametlh 377
 QY 343 AEKREDLTLTHFDYRKDWESFLEALRTSPGVTGPVREYNERNKANILINQFOLQOME 402
 Db 378 assrhqiridfnrdhtlgrilnametnffvgvqvfvnfermgtkfkfqqdsrev 437
 QY 403 KIGYHSQKSLDLSLGPKVWVGKTPPKDRTLIIYIEHSQVNPITYIVSASASVIGVITA 462
 Db 438 kvgeynavadtlei-indtirfgseppkktlileqkrkislphysilsaltlilgmima 496
 QY 463 TVFLAFNKNRYNQRKMSPHLNLIIIVGCMITYLSIIFGLDPTLSSVAAPFYICTAR 522
 Db 497 safilfnknrnqklknsspymnliilgmsyasiflglgdsfvsektfetlctvr 556
 QY 523 AWILMAGFSLSGAMFSTWVHSTFTDLKLNKKVYKQLEPMVGVVLLAIDIAITWQ 582
 Db 557 twiltvgyttafgamlfaktvrvhaifnvmkkmkklkqdkilvlggmllidlcilicwq 616
 QY 583 IADPFYR--ETKQLEPLHENID-----DVLVIPENEYQSEHMTTFVSIYAYKGLLVF 636

Db 617 avoplrtrtvekysmep-----dpagrdisirpllecenthmtiwigivaykglmlf 670
 QY 637 GAFLAWETRHSVPALNDSKHIGFSYVNVFITCLAGAAISLVLSDRKDLVFLVLSFFIIF 696
 Db 671 gcflawetrnvspalndskysvnygmciigaavsflltrdgnvqfcaivalviif 730
 QY 697 CTTATLCLVFVKLVKELKRNPOGVV-DKRVRAIIRPMKNGRRDSSVCELEQ-----RLRD 751
 Db 731 csttitclvfpklitlrtnpdaatqnrrfqtgnqkckedsktstsvtnqastslreg 790
 QY 752 VNTNCRFRKALMEKENELOALIRKL--GPEARKWIDGVCTCGSNVGSLEPILNDDIV 809
 Db 791 lqsenhrimkitelkdleevtmqtdtpekttyik-----qnhyqelndiln---- 839
 QY 810 RLSAPPVRREMPSTTVEMT-SVDSVTSTHIVENDNSFVSQSVTMAPSLPPKKKQSIVE 868
 Db 840 -----lgnfstedggkalknhldqn-----pqj-----q 865
 QY 869 HHSHAPAPTMQPIQO-QLQHQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQHQQH 927
 Db 866 wnttepsrtckdpiedinspehigrirlslqlpil-----hhayl----- 904
 QY 928 SVSAQVDDNIGSITSTAGKRSGDCSSMRERRROSTASRHYDSGSQTPPTARPKYSSSHRNS 987
 Db 905 -----psiggyv-----dascvspcvspstasprhrv 930
 QY 988 STNISTSQSELSN 1000
 Db 931 ppsfrvmvsglsd 943

RESULT 3
 AAY29796
 ID AAY29796 standard; Protein; 941 AA.
 AC AAY29796;
 DT 15-NOV-1999 (first entry)
 XX Human gamma-amino-butyric acid B receptor subunit HG20.
 KW Gamma-amino-butyric acid B receptor subunit; HG20; GABABR1a;
 KW depression; epilepsy; neuropsychiatric disorder; dementia;
 KW muscular contraction; central nervous system disorder.
 OS Homo sapiens.
 XX WO9940114-A1.
 XX 12-AUG-1999.
 PF 03-FEB-1999; 99WO-US02361.
 XX 05-FEB-1998; 98US-0073767.
 XX (MERI) MERCK & CO INC.
 PA (MERI) MERCK FROSST CANADA INC.
 PA (UYTE-) UNIV TEXAS HEALTH SCI CENT SAN ANTONI.
 XX (USSH) US NAT INST OF HEALTH.
 PI Bonner TI, Bonnert TP, Clark J, Kolakowski LF, Liu Q;
 PI McDonald T, Ng GYK;
 XX WPI; 1999-527300/44.
 DR N-PSDB; AA206968.
 XX New DNA encoding human and murine receptor subunits, useful for
 PT identifying agonists and antagonists for treatment of depression,
 PT epilepsy and neuropsychiatric disorders
 XX Claim 7; Fig 2; 128pp; English.

XX Claim 2; Page 32-39; 62pp; German.
XX This invention describes a novel polypeptide (I), functioning as a
CC gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal
CC activity. (I), also the nucleic acid (II) that encodes it and related
CC vectors, host cells, antibodies and transgenic invertebrates, are used
CC for identifying: (i) new plant protection agents, i.e. modulators of (I),
CC with insecticidal activity, which may also be useful in human or
CC veterinary medicine; and (ii) genes that encode polypeptides involved in
CC assembly of functionally related GABA-B receptors in insects. This
CC sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor
CC which is described in the method of the invention.
XX Sequence 1220 AA;
XX
Query Match 100.0%; Score 6409; DB 22; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MFRPSFPFASLLELLWSTACGRTAKRSDVYIAGFFPYGDGVNSYTGKVPMSVKLAL 60
DB 1 MFRPSFPFASLLELLWSTACGRTAKRSDVYIAGFFPYGDGVNSYTGKVPMSVKLAL 60
QY 61 GHVNEHGKILANYRLHWNNDTCGNAAGVGVKSPFDMHSGPNKVMFLGCACTHVDPIAK 120
DB 61 GHVNEHGKILANYRLHWNNDTCGNAAGVGVKSPFDMHSGPNKVMFLGCACTHVDPIAK 120
QY 121 ASKHWHLTQLSYADTHPMFKDAPPNFRVVPSENAFNAAPRLALLKEFNTRVGTVYONE 180
DB 121 ASKHWHLTQLSYADTHPMFKDAPPNFRVVPSENAFNAAPRLALLKEFNTRVGTVYONE 180
QY 181 PRYSLPHNMVADLDAMEVEVWETQSFVNDVAESLKLREKDVRIILGNFNEHFAKAFK 240
DB 181 PRYSLPHNMVADLDAMEVEVWETQSFVNDVAESLKLREKDVRIILGNFNEHFAKAFK 240
QY 241 EAYKLMYGRAYOWLIMATYSTDMWNVQDSECSVEIATALEGAILVDLLPLSTSGDIT 300
DB 241 EAYKLMYGRAYOWLIMATYSTDMWNVQDSECSVEIATALEGAILVDLLPLSTSGDIT 300
QY 301 VAGITADEYLVEYDRRGTEYSFHHGYTDGIWAAALAIQYVAEKREDLLTHFDYRVKDW 360
DB 301 VAGITADEYLVEYDRRGTEYSFHHGYTDGIWAAALAIQYVAEKREDLLTHFDYRVKDW 360
QY 361 ESFVLEALRNTSEGTGTPVRFYNNERKANILINQFOLGOMEKIGEYHSOKSHLDLSLIGK 420
DB 361 ESFVLEALRNTSEGTGTPVRFYNNERKANILINQFOLGOMEKIGEYHSOKSHLDLSLIGK 420
QY 421 PVKWGKTPPKDRTLIIYIEHSQVNPITYIVSASVIGVIIATVFLAFNIKYNQRIYKM 480
DB 421 PVKWGKTPPKDRTLIIYIEHSQVNPITYIVSASVIGVIIATVFLAFNIKYNQRIYKM 480
QY 481 SSPHLNLIIVGCMITYLSIIFGLDITLSSVAAPFICTARAWILMAGFSLSGAMFSK 540
DB 481 SSPHLNLIIVGCMITYLSIIFGLDITLSSVAAPFICTARAWILMAGFSLSGAMFSK 540
QY 541 TWRVHSIFDCLKNKVKIKDYQLFVVGVLADIAITTTQIATWQADPPYRETQLEPLHHE 600
DB 541 TWRVHSIFDCLKNKVKIKDYQLFVVGVLADIAITTTQIATWQADPPYRETQLEPLHHE 600
QY 601 NIDVDLVIPENECYQSEHMTIFVSIYAYKGLLVGAFIATWETRHVSIPALNDSKHIGF 660
DB 601 NIDVDLVIPENECYQSEHMTIFVSIYAYKGLLVGAFIATWETRHVSIPALNDSKHIGF 660
QY 661 SYNVNFTITCLAGAAISLVLSDRKDLVFLSFFIICCTTATLCLVFPKLVKLRNPGV 720
DB 661 SYNVNFTITCLAGAAISLVLSDRKDLVFLSFFIICCTTATLCLVFPKLVKLRNPGV 720
QY 721 VDKRVVATLRPMKNGRRDSSVCELEQRDLVDKNTCRFRKALMEKENELQALIRKIGPE 780
DB 721 VDKRVVATLRPMKNGRRDSSVCELEQRDLVDKNTCRFRKALMEKENELQALIRKIGPE 780

QY 781 ARKWIDGVTCTGGSNVGSELEPILNDDIVRLSAPPVRRREMPSTTVMETSVDSVTSHVE 840
DB 781 ARKWIDGVTCTGGSNVGSELEPILNDDIVRLSAPPVRRREMPSTTVMETSVDSVTSHVE 840
QY 841 MDNSFVSQSTVMAPSLPPKKKQSTVEHHSHAPAPTMOPIQOOLQOHLQOHOQOQOH 900
DB 841 MDNSFVSQSTVMAPSLPPKKKQSTVEHHSHAPAPTMOPIQOOLQOHLQOHOQOQOH 900
QY 901 LQOQOHOQOQOQOQOQOHHHRLKRNVSQAOTDDNIGSITSTAGKSGGDCSSMRERQ 960
DB 901 LQOQOHOQOQOQOQOQOHHHRLKRNVSQAOTDDNIGSITSTAGKSGGDCSSMRERQ 960
QY 961 STASHYDSGOSTPAPRKYSSSHRSNSTNISTSOSELSNMCPSHPKSTPAVIKTPASD 1020
DB 961 STASHYDSGOSTPAPRKYSSSHRSNSTNISTSOSELSNMCPSHPKSTPAVIKTPASD 1020
QY 1021 HRRITSMGSAKSNFVVSQSLDWDTHLTHAKORQSPRYASPORCAEHGHGMYDPNT 1080
DB 1021 HRRITSMGSAKSNFVVSQSLDWDTHLTHAKORQSPRYASPORCAEHGHGMYDPNT 1080
QY 1081 TSPIQRSVSEKNNRHRPKQKGTVCQSETDSEDERDPPNSQPCVQPKVSRSSNIQHA 1140
DB 1081 TSPIQRSVSEKNNRHRPKQKGTVCQSETDSEDERDPPNSQPCVQPKVSRSSNIQHA 1140
QY 1141 AHHISSPNVADPKQRSORQKQDSSIIYGASSETELLEGETAILPIFRKLLTEKSPNYRGR 1200
DB 1141 AHHISSPNVADPKQRSORQKQDSSIIYGASSETELLEGETAILPIFRKLLTEKSPNYRGR 1200
QY 1201 SAVGSCPNISIKCDIVEYL 1220
DB 1201 SAVGSCPNISIKCDIVEYL 1220
RESULT 2
AA28837
ID AAY28837 standard; protein; 943 AA.
XX
AC AAY28837;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human GABABR2 receptor protein.
KW Human GABABR2 receptor protein; human gamma-aminobutyric acid receptor;
KW metabotropic receptor; synaptic transmission; antibody; spasticity;
KW recombinant nucleic acid technique; motor control disorder;
KW therapeutic modulator; GABABR2 quantification; affinity purification.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 13 /note= "Corresponds to cng codon"
FT Misc-difference 942 /note= "No corresponding codon in seq ID no.1"
FT Misc-difference 943 /note= "No corresponding codon in seq ID no.1"
FT Domain 1, 422
FT /label= Extracellular_domain
FT /note= "can be swapped with the portions of calcium
FT receptor for measurement of antagonist activity"
FT Domain 423..686
FT /label= Transmembrane_domain
FT Domain 687..883
FT /label= Intracellular_domain
FT /note= "can be swapped with the portions of calcium
FT receptor for measuring intracellular effects"
PN WO9951636-A2.
XX
XX 14-OCT-1999.
XX
XX 02-APR-1999; 99WO-US07352.
PF

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 09:50:57 ; Search time 52.81 Seconds
(without alignments)
1711.218 Million cell updates/sec

Title: US-09-715-962-4

Perfect score: 6409

Sequence: 1 MFRPSWFPASLFLLLNST.....SAVGQSCPNSIKCDIVEYL 1220

Scoring table:

BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6409	100.0	1220	22 AAB86160	D. melanogaster GA
2	1602	25.0	943	20 AAY28837	Human GABABR2 rece
3	1598	24.9	941	20 AAY29796	Human gamma-amino
4	1598	24.9	941	21 AAW90938	Human GABA-B recep
5	1598	24.9	941	21 AAY51928	Human GABA-B recep
6	1598	24.9	941	21 AAY70328	Human GABA-B-R2 re
7	1598	24.9	941	21 AAY79202	Human GABAB recep
8	1598	24.9	941	21 AAY44342	Human gb2 GABA B r
9	1598	24.9	941	22 AAB50088	HG20 protein seque
10	1597	24.9	941	21 AAY68743	A human gamma-amin
11	1596.5	24.9	914	21 AAY44344	Protein-1 related

12	1593	24.9	1303	20	AAY49132	GABA-BR2*Gqo5 fusi
13	1591.5	24.8	965	21	AAV44345	Protein-2 related
14	1590	24.8	898	20	AAV14082	Human GABABR2 prot
15	1590	24.8	898	21	AAW70326	Human gamma amino
16	1582.5	24.7	940	21	AAW90937	Rat GABA-B recepto
17	1582.5	24.7	940	21	AAY70327	Rat gamma amino bu
18	1581.5	24.7	940	21	AAY51927	Rat GABA-B recepto
19	1579.5	24.6	940	21	AAV44343	Rat gb2 GABA B rec
20	1561	24.4	883	20	AAV14081	Rat GABABR2 protei
21	1442.5	22.5	859	20	AAV34111	Human GABA recepto
22	1442.5	22.5	859	20	AAV30311	Amino acid sequenc
23	1442.5	22.5	874	20	AAY29661	Human 7TM receptor
24	1249	19.5	659	22	AAB50094	GB2 protein. Cagn
25	1229	19.2	1305	22	AAB86161	D. melanogaster GA
26	1186.5	18.5	840	22	AAB86159	D. melanogaster GA
27	1166.5	18.2	1323	20	AAY49133	GABA-BR1a*Gqo5 fus
28	1155.5	18.0	960	19	AAW40116	Rat GABA-BR1a rece
29	1155.5	18.0	960	22	AAB50089	Murine GABA-B-R1a.
30	1154.5	18.0	960	22	AAY29797	Murine gamma-amino
31	1154	18.0	962	22	AAB50090	Human GABA-B-R1a.
32	1152	18.0	844	19	AAW40118	Rat GABA-BR1b rece
33	1151.5	18.0	960	21	AAV83145	Human GABAB1AA rec
34	1151.5	18.0	961	20	AAY28838	Human GABABR1a rec
35	1151.5	18.0	961	20	AAY29798	Human gamma-amino
36	1151.5	18.0	961	20	AAV14101	Human GABAB recep
37	1149.5	17.9	960	20	AAY28841	Rat GABABR1a rece
38	1149.5	17.9	960	20	AAY49122	Rat GABABR1a prote
39	1148	17.9	844	19	AAW40119	Human GABA-BR1b re
40	1148	17.9	844	20	AAY28839	Human GABABR1b rec
41	1148	17.9	844	20	AAV14102	Human GABAB recep
42	1148	17.9	844	21	AAV32467	Human G-protein co
43	1148	17.9	899	20	AAV14107	Human GABAB recep
44	1146	17.9	844	20	AAY28842	Rat GABABR1b rece
45	1146	17.9	844	20	AAY49123	Rat GABABR1b prote

ALIGNMENTS

RESULT 1
AAB86160
ID AAB86160 standard; Protein; 1220 AA.
XX
AC AAB86160;
XX
DT 03-AUG-2001 (first entry)
XX
DE D. melanogaster GABA-B receptor protein SEQ ID 4.
XX
KW GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor;
KW insecticide; transgenic invertebrate; plant protection agent;
KW human medicine; veterinary medicine; insect.
XX
OS Drosophila melanogaster.
XX
PN DE19955408-A1.
XX
PD 23-MAY-2001.
XX
PF 18-NOV-1999; 99DE-1055408.
XX
PR 18-NOV-1999; 99DE-1055408.
XX
PR (FARB) BAYER AG.
XX
PI Raming K, Mezler M, Mueller T;
XX
DR WPI: 2001-318282/34.
DR N-PSDB; AAH20520.
XX
PT New invertebrate gamma-aminobutyric acid receptor proteins, useful in
PT screening for potential insecticides, for plant protection or medicine,
PT also related nucleic acid

Query Match 4.4%; Score 280.5; DB 2; Length 915;
Best Local Similarity 20.7%; Pred. No. 3.5e-15;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;

QY 7 FPFASLFLLLWSTACGRYAK-----RSDVYIAGFPY-YGDGVENSYTG-----RG 51
DB 16 FPCCVLEVLCLVLAARQGEYAPHISIRIEGDTVIGGLFPVHAKGSPGCPGDIKRENG 75
QY 52 V--MPSVKIALGHVNEHGKILANYRLHMMNDTCNAAVGVKSFDDMMHS----- 99
DB 76 IHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDTYALEQSLTFVQALIQKDTSDVR 135
QY 100 -----GPNKVM-LFGAACTHTDPTIAKSKHHLTQLSYADTHPMFTKDAFPNFF 148
DB 136 CTNGEPPVFEVPEKVVGVIGAGSSVIMVANILRLFIQIISYASTAPELSDDRRYDF 195
QY 149 -RVVPSENAFNAPRLALKKEFNTRVCTVYQNEPRYS----- 184
DB 196 SRVPPDSFQAQAMVDIVKALGWNVYSTL-ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKLREKDVRIILGNFNEHFA 235
DB 255 RIPOERKRTIDFDRIIKQLLDPNSRAVVIFAND-----EDIKQIL----- 296
QY 236 RKAFCAYKLDYGRAYQWLMATYSTDMWNTQDSECSVEEIIATALEGAILVDLLPLST 295
DB 297 ----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGAITIQPKRATV 343
QY 296 SG-----DITVAGI---TADYILVEYDRL-RGTEYS 322
DB 344 EGFDAYFTSRTLENNRNWFAFYWEENFNCKLTISGSKKEDTDKCTQGERIGKDSNYE 403
QY 323 RFHG-----YTYDGIWAAALAIQYVAEKREDLLTHFYDR--VKDWESV-----FLEALRNTSF 373
DB 404 Q-EGKVQFVIDAYAMAHALHM--NKDLCA--DRGVCPEMEQAGCKLLKYIRHVNF 457
QY 374 EGVGTG-PVRF-YNNERKANILNQFOLGQMEK-----IGEY--HSQKSHLDLSLGKPKVK- 423
DB 458 NGSAGTPVMFNKNGDAPGRYDIFQYQTTNTTNPGRIGQWTDQLNLNIEDMQWKGKGVRE 517
QY 424 -----WV-----GKTPPKDRT--- 434
DB 518 IPSSVCTLPCKPQQRKTKGTCCWTCPCDGYQYQFDEMTQHCPCPYDQRPENRTGCQ 577
QY 435 ---LIYIE-HSOVNPTIYIVSASVIGVITATVE-LAFENIKYRNQRYIKMSSPHLANLI 489
DB 578 NPIPIKLEWHS-----PWAVIPVFLAMLG-IATFVMTATFIRYNDTPIVRASGRELSYVL 632
QY 490 IVGCMITYLSIIFGLDFTLSSVAAFP--YICTARAWILMAGFSLSGAMFSKTRVHSHI 547
DB 633 LGIFLCYI-ITFL-----MIAPDVAVCSFRRVFLGLGMCISYAALLTKTNRIYRI 683
QY 548 FTDLKLN---KKVIKDYQLPMVGVVLLAIDIAITTWQIADP-----FYRETKOLEPLHH 599
DB 684 FEQGGKSVTAPRLISPTSQLAITSLSISVQLLGVFIWFGVDPNIIIDYDEHKTMNP--- 740
QY 600 ENIDDDVLVIPENYCOSEHMTIFVSIYAYKGLLVFGAFANETRVHSIPALNDSKHIG 659
DB 741 EQARGVL-----KCDITDQIICSL--GYSILLWVTCTVYAIKTRGVF-ENFNEAKPIG 791
QY 660 FSVYNVFIITCLAGAAISLVLSDRKDLVFF--LISFFIIFCTTATLCLVFVPKLVKLKRN 716
DB 792 FTMYTTCIVWLAFPIFFGTAQSAEKLYIQTTTLTISMNLSASVALGMLYMPKYVYIIFH 851
QY 717 POGVVDKRVRA-----TLRPMK-----NGRRDSSVCE 744
DB 852 PELNVQKRKRKRAVVTAAATMSSRLSHKSPDRPNGEAKTELCE 894

```

; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,862
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,401
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-18-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 915 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-453-862-2

Query Match 4.4%; Score 280.5; DB 1; Length 915;
Best Local Similarity 20.7%; Pred. No. 3.5e-15;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;

QY 7 PFEASLLFLWSTACGGTAK-----RSDVYIAGFEP-YGPGVENSYTG-----RG 51
DB 16 FPCCVLEVLVCVLAARQGEMYPAPHSTRIGDVTGLGLFPVHAKGSPGCPGDIKRENG 75
QY 52 V--MPSVKALGHNVEHGKILANTRLHWNWNDTCNAAVGVKSPFDDMHSS----- 99
DB 76 IHRLEAMLYALDQNSDPNLLPNVTLGARILDTCSRDIYALEQSLTFVQALLTKDTSVDR 135
QY 100 -----GPNKVM-LFGAACHVTDPIDAKASKWHHLTQLSYADTHPMFTKDAFPNPF 148
DB 136 CTNGEPPVFVPEKPVGVIGASGSSVTMWANILRLFOIQISYASTAPELSDRRYDFF 195
QY 149 -RVYPSNAFNAPRLALKKEFNWTRVGVYQNEPRYS-----184
DB 196 SRVYPPDSFOAQAMVDIVKALGNWVSTL-ASESGYGEKGVESFTQISKEAGGLCIAOSV 254
QY 185 -LPNH--MVADLDAMEVEVYVETOS-----FVNDVAESLAKLRKEDVRIILGNFNEHFA 235
DB 255 RIPOEKDRDTIDFDRIIKQLDTPNSRAVIFAND-----EDIKQIL----- 296
QY 236 RKAFCEAYKLDYGRAYQWNLIMAYYSTDMWNVTQDSECSVEIATALEGAILVDLLPLST 295
DB 297 ---AAAKRADQVGH-FLWV---GSDSWGSKINPLHQHEDIA---EGAITIQPKRATV 343
QY 296 SG-----DIIVAGI---TADEYLVEYDRL-RGTYS 322
DB 344 EGFDAFTTSRLNNRRNVWFAEYWEENFNCKLTISGSKKEDTRDKCTGCGRIKGSNYE 403
QY 323 RFHG---YTYDGIWAAALAIQYVAEKREDLLTHFDYR--VKDWESV----FLEALRNTSF 373
DB 404 Q-EGKVQFVIDAVYAMAHALHHM---NKDICA--DYRGVCPMEQAGGKLLKYIRHWNF 457
QY 374 EGVGTG-PVRF-YNNERKANILLINQFQGMKEK-----IGEY--HSQKSHLDLSLQKPKV- 423
DB 458 NGSAGTPVMFNKNGDAPGRYDFIQYQTNTTNPGRVLLIGQWTDLQLNIEDMQWCKGVRE 517
QY 424 -----WV-----GKTPPKDRT--- 434
DB 518 IPSSVCTLPCKPGQRKKTQKTPCCTCEPCDGYQYQFDEMTQCHQCPDYDRPNENRTGCQ 577

```


; TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds

; FILE REFERENCE: 4-19679/A/PCT
; CURRENT APPLICATION NUMBER: US/08/617,785E
; CURRENT FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: PCT/EP94/02991
; EARLIER FILING DATE: 1994-09-07
; EARLIER APPLICATION NUMBER: EPO 9416553.7
; EARLIER FILING DATE: 1994-08-19
; EARLIER APPLICATION NUMBER: EPO 93810663.0
; EARLIER FILING DATE: 1993-09-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 922
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-617-785-14

Query Match 4.5%; Score 290.5; DB 4; Length 922;

Best Local Similarity 20.8%; Pred. No. 4.8e-16;

Matches 199; Conservative 145; Mismatches 337; Indels 275; Gaps 49;

QY 7 FPPASLLFLLLWSTACGRTAK-----RSDVYIAGFFP-YGDGVENSYTG-----RG 51
DB 16 FPCCVLEVLICALAAARGQEMYPHPSIRIEGDTLGLFPVHAKGSPGVCDDIKRENG 75
QY 52 V--MPSVKALGHVNEHGKILANRLHMMWNTQCNAAVGVKSFDDMMHS-----99
DB 76 IHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDTYALVQSLTFVQALIQKDTSDVR 135
QY 100 -----GPNKVM-LFGAACHTVTDPIAKASKHHLTQLSYADTHPMTKDAFPNFF 148
DB 136 CTNGEPPVFKVPEKVVGVIGAGSSVSIWANILRLFQIPQISYASTAPSELSDDRRYDF 195
QY 149 -RVVPSNAPNAPRLALKKEFNWTRVGVYQNEPRYS-----184
DB 196 SRVVPDPSFOQAQMVDIKALGNVYVSTL-ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKKLRKDVRIILGNFNEHFA 235
DB 255 RIPOERKDRITDFRIKQLDTPNSRAVIFAND-----EDIKQIL-----296
QY 236 RKAFCAYKLDYGRAYQWLMATYSTDMWNTQDSECSVEEATALEGAILVDLLPLST 295
DB 297 ----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGAITIQPKRAIV 343
QY 296 SG-----DITVAGI---TADYLVYEDRL-RGTEYS 322
DB 344 EGFDAYFTSRTLNNRRNVWFAEYWEENFNCKLTISGSKKEDTDKCTGQERIGKDSNYE 403
QY 323 RFHG---YTDGIWAAALAIQYVAEKREDDLLTHFDYR--VKDWESV---FLEALRNTSF 373
DB 404 Q-EGKVQFVIDAVYAMAHALHHM---NKDLCA--DYRGVCPMEQAGKKLLUKYIRNVNF 457
QY 374 EGVRG--PVRF--YNNERKANILINQFQAGMEK-----ICEY--HSQKSHLDSLAKPVK- 423
DB 458 NSGAGTPWMENKNGDAPGRYDFIQYTTNTSNPGYRLIGQWTDQLNLNEDQWQGVRE 517
QY 424 -----WV-----GKTPPKDRT-----434
DB 518 IPASVCTLPCKPGORKKTKQKTPCCWTCPCDGYQYQFDEMFTCOHCPYDQRPENRTGQ 577
QY 435 ---LIYIE-HSOVNPTIIVSASVIGVIATV-F-LAFNIKYRQRYIKMSSPHLNL 489
DB 578 DIPILKEWHS-----PWAVIPVFLAMLG-ITATIEVMTAFIRYNDTPIVRSGRELSYVL 632
QY 490 IVGCMITYLSIFIQLDITLSSVAAPP--YICTARAWILMAGFSLSGFAMFSKTRVHSH 547
DB 633 LTGIFLCYI-ITFL-----MIAKPDVAVCSFRVFLGLGMCISYAALLTKTRIYRI 683
QY 548 FTDLKLN---KKVTKDYOLFVWVGVLIAIDIAITWTQIADP-----FYRETKQLEPLHH 599

DB 684 FPGKKSVTAPRLISPTSQLATSSLSVQLLCGVFIWFGVDPNPNIIDYDEHKTMP--- 740
QY 600 ENIDDDVLVIPENEYCOSEHMTIFVSIYAYKGLLVFGAFLAWETHRVSVIPALNDSKHIG 659
DB 741 EQARGVL-----KCDITDLQIICSL--GVSILLMVTCTVYAIKTRGVP--ENENEAKPIG 791
QY 660 FSVYVNFITCLAGAAISLVLSDRKDLVTV---LLSFFIIFCTTATLCLVFPVKLVKRN 716
DB 792 FTMVYTCIVMLAFIPFIFFGTAQSAEKLYIQTTTLTISMNLSASVALGMLYMPKVIIFH 851
QY 717 POGVVDKRVRA-----TLRPMK-----NGRRDSSVCELEQRLRDVKNTNC 757
DB 852 PELNVOKRRSRFKAUVTAATMSRSLSHKPSDRPNGEAKTELCE-----NVDNNC 901

RESULT 11

US-08-617-785-12
; Sequence 12, Application US/08617785E

; Patent No. 6228610

; GENERAL INFORMATION:

; APPLICANT: Flor, Peter J.

; APPLICANT: Kuhn, Ranier

; APPLICANT: Lindaur, Kristen

; APPLICANT: Puttner, Irene

; APPLICANT: Knopfel, Thomas

; TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4,
; FILE REFERENCE: 4-19679/A/PCT

; CURRENT APPLICATION NUMBER: US/08/617,785E

; EARLIER FILING DATE: 1996-03-19

; EARLIER APPLICATION NUMBER: PCT/EP94/02991

; EARLIER FILING DATE: 1994-09-07

; EARLIER FILING DATE: 1994-08-19

; EARLIER APPLICATION NUMBER: EPO 93810663.0

; EARLIER FILING DATE: 1993-09-20

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 915

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-617-785-12

Query Match 4.5%; Score 286.5; DB 4; Length 915;

Best Local Similarity 20.8%; Pred. No. 1.1e-15;

Matches 196; Conservative 144; Mismatches 334; Indels 269; Gaps 48;

QY 7 FPPASLLFLLLWSTACGRTAK-----RSDVYIAGFFP-YGDGVENSYTG-----RG 51
DB 16 FPCCVLEVLICALAAARGQEMYPHPSIRIEGDTLGLFPVHAKGSPGVCDDIKRENG 75
QY 52 V--MPSVKALGHVNEHGKILANRLHMMWNTQCNAAVGVKSFDDMMHS-----99
DB 76 IHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDTYALVQSLTFVQALIQKDTSDVR 135
QY 100 -----GPNKVM-LFGAACHTVTDPIAKASKHHLTQLSYADTHPMTKDAFPNFF 148
DB 136 CTNGEPPVFKVPEKVVGVIGAGSSVSIWANILRLFQIPQISYASTAPSELSDDRRYDF 195
QY 149 -RVVPSNAPNAPRLALKKEFNWTRVGVYQNEPRYS-----184
DB 196 SRVVPDPSFOQAQMVDIKALGNVYVSTL-ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKKLRKDVRIILGNFNEHFA 235
DB 255 RIPOERKDRITDFRIKQLDTPNSRAVIFAND-----EDIKQIL-----296
QY 236 RKAFCAYKLDYGRAYQWLMATYSTDMWNTQDSECSVEEATALEGAILVDLLPLST 295
DB 297 ----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGAITIQPKRAIV 343

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; TITLE OF INVENTION: CHIMERIC RECEPTORS AND METHODS FOR
; IDENTIFYING COMPOUNDS ACTIVE AT
; TITLE OF INVENTION: METABOTROPIC GLUTAMATE RECEPTORS AND
; TITLE OF INVENTION: THE USE OF SUCH COMPOUNDS IN THE
; TREATMENT OF NEUROLOGICAL DISORDERS
; TITLE OF INVENTION: AND DISEASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,289A
; FILING DATE: July 25, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,526
; FILING DATE: July 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 220/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1056 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-687-289A-8

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Query Match	4.6%	Score 295.5;	DB 2;	Length 1056;
Best Local Similarity	17.9%	Pred. No. 2.2e-16;		
Matches 221;	Conservative 170;	Mismatches 360;	Indels 481;	Gaps 52;

QY	23	GR	TAKRS	-----DVYIAGFF-----PYGDGVNSY	TGR-----GV--MPSYKALGHVN	64
				: : :	: : :	
Db	31	GA	SSORVARMDG	DVIIIGALFVHHQPPAEKVP	PERKCGEIRBQYGIQIRVEAMFHTLDKIN	90
				: : :	: : :	
QY	65	EH	KKILANLYLH	WVNDTCQNAAVGVKSFFDMH	-----SGPNKM-----	105
				: : : : :	: : :	
Db	91	AD	PVLLPNTIT	LGSEIRDSCHWSSVALEQSEIT	IRDSLISIRDEKDLNCLPDGOTLP	150
				: : :	: : :	
QY	106	-----	LFGA	ACTVTDPIAKASKHWHLTQ	LSYADTH-PMETKDAFFNFRVVP	156
				: : :	: : :	
Db	151	RT	KKPIAGV	IGPGSSVAIQVNLQLFDIP	QIAYSATSIDLSDKTLYKYFLR	210
				: : :	: : :	
QY	157	FN	APRLLALKE	FNWTRVGYQNEPRYSLPHNH	WADLDAME-VEVETOSFVNDVAES	214
				: : :	: : :	
Db	211	QA	RAML	DIVKRYNWTYSAVH-TEGNY	GSQMDAFELAQAQGLCIAHSDKI	269
				: : :	: : :	
QY	215	-----	LKKLREK	--DVRILIGNFNEHFAKAFCEAY	-----KLDMYGRAYOWLIMA	258
				: : : :	:	
Db	270	FD	RLLRKLRE	PLKARVV-----CFCEG	MVTRGLLSAMRELGVVGE-----	313
				: : :	: : :	
QY	259	TY	STDWNV	TQDSECSVEEIAFAL	EGAILVDL-----LPJSTSGDIT	304
				: : :	: : :	
Db	314	LI	GS	DG---ADRDEYIEGVE	EVANGIITIKQSPERSFDDYFKLR	362
				: : :	: : :	

TITLE OF INVENTION: AND DISEASES
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/687,289A
 FILING DATE: July 25, 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/001,526
 FILING DATE: July 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 220/004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1219 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-687-289A-6

Query Match 4.6%; Score 297; DB 2; Length 1219;
 Best Local Similarity 18.3%; Pred. No. 2.1e-16;
 Matches 247; Conservative 189; Mismatches 449; Indels 466; Gaps 59;

QY 12 LFLFLWSTAC-----GRTAKRSDVYIAGFPYGDGVENS-----YTGRGV 52
 DB 9 VLLALTWHFSAYGPDORAKKGGDIIIGGLPFIHGVAAKQDQDLKSRPESVECIYRNGRF 68
 QY 53 --MPSYKLAGHVNHEGKILANRLHMMWMDTQCA-----AVGVKS 92
 DB 69 RWLQAMIFAIEEINSSPALLPNTLTGYRIFDT-CNTVSKALEATLSFVAQNKIDSLNIDE 127
 QY 93 FDMHISGKNVLMFGAACHVTDPTAKASKHHULTQLSYADTHPMT-KDAPNFFRV 151
 DB 128 FNCSEHIPSTIAVVGATGSGVSTAVANLGLFYPOVYASSRLLSNKQKSFRLTI 187
 QY 152 PSENAFNAPRLALKFENFTRVGTVQNEPRYSLPH----- 187
 DB 188 PNDEHQATAMADIIIEFRNWVGITIAADD-YRPGTEKPEEAERDIDCFSELISQY 246
 QY 188 -----NHMVADLDAMEVEYVTSQSFVNOVAESLKLKREKV----- 223
 DB 247 SDEEIQHVVEVQNSTAKVIVVFSSGPDLEPLIKEIVRNTCKIWLASEAWASSLIA 306
 QY 224 -----RIILGNFNEHFAKA-----FCEAYKLDWYGRAYOWLMATYSTDMWNTQDSEC 273
 DB 307 MPOYFHVVGIGTIC--FALKAGQIPGREFLK-KVHPRK---SVHNGFAKEFWEET--FNC 358
 QY 274 SVEEITALEGALVDLL-----PLSTSGDITVAGITADELYVEYD 314
 DB 359 HLOEGA---KGPLPVDFTFLRGHEESGDRFSNSTAFRPLCT-GDENISSV--ETPYIDYT 412

QY 315 PLRGTEYSRPHGYTYDGIWAAALAIQ--YVAEKREDLLTHFD-----YRVKDWESVLEAL 368
 DB 413 HLR-ISYN-----VYLAVYSTAHALQDIYTCPLGRGLFTNGSCADIKKVEAMQ--VLKHL 464
 QY 369 RNTSFEQVGTG-----PVRFYN-----N 385
 DB 465 RHLNFTNMGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGYNNYAKKGERLFIN 524
 QY 386 ERKANILINOFQ-----LGOMEKI-----GEYHSOKSHLDL 416
 DB 525 EEK--ILWSGFSREVPFNSCRDCLAGTRKGIIEGEPTCCPEVCBPDEGYSDETDASAC 582
 QY 417 SLGKPVKWKVK--TPPKDRTLIYIHSQVNPITYIVTSASVIGVILITVFLAFNIKVRN 474
 DB 583 NKCPDDFWSNENHTSCEPIPVRYLEWSDIES---IIAFAFSLGILVTLFVLFLIEVLVYRD 639
 QY 475 QRYIKMSSPHLNNLIIVGCMITYLSIIFGLDITLSSVAAPFYIC-----TARAWI 525
 DB 640 TPVVKSSRELCYIILAG-----IFLG-----YVCPFTLIAKPTTTCYL 679
 QY 526 --LMAGFS--LSFGAMFSKTRVHSIFTDLKNKKVVKDYQLFM-----VGVLLAID 574
 DB 680 QRLVLGLSSAMCYSAVTKTNRIARILAGSK--KICTRKPRMSAWAQVILIASILISVQ 737
 QY 575 IAITTWOIADFPYRETROLEPHHENIDDLVIVIPENYCOSEHMTIFVSIYAYKGLLL 634
 DB 738 LTLVTLIIMEP-----PMPILSYPSIKEVLI-----CNTSLGVVAPV--GYNGLLI 784
 QY 635 VFGAFLAWEETHVSIIPA-LNDSKHIGFSVYVNFITCLAGAAISLVLSRDKDLVFLVLSFF 693
 DB 785 MSCTYYAEKTRNV--PANFNEAKYIAFTMYTTCIILWAFVIYF-----GSNYKIITTCFA 838
 QY 694 IIFCTTATLCLVFPKVLKRNPOGVVDKVRRAFL----- 729
 DB 839 VLSVTVALGCMFTPKWYIIIAKP-----ERNVRSFTTSDVVRMVGDKLPCRNTFLN 894
 QY 730 -----RPMKNGRRD--SSVCELEQRDLV-KNTNCRFRKALMEKNEL---QALIRKLG 778
 DB 895 IFRKKKPGAGNANSNGKSVSWSEPGGRQAPKQGHVWQRLSVHVKTNETACNTACNTAVIKPLT 954
 QY 779 PEARKWIDGVTCGS-----NVGSE-----LEPILNDDIVRLSAPPVREMPSTTV 825
 DB 955 KSYOGSGKSLTFSDASTKTLNVEEEDNTPSAHSPSPSPSMVHRRGPPVATTTP----- 1010
 QY 826 TEMTSVDVSTVTHVMDNSFVSQSTVMAPSLPPKKKKQSVIEHSHAPATMMQPIQO- 884
 DB 1011 -----LPHLTAETPLFLADSVIPKGLPPLPQO-----QFOQPPPPQPPQ 1054
 QY 885 -QLQOHLQ-----QHOOQOQOHLQOQOQH 906
 DB 1055 KSLMDQLQGVVTFNFGSGIPDFHVLAVLAGPCTPGNSLSRLYPPPPPHQLQMLPLHLSTQEQ 1114
 QY 907 QOMQOQOQOQOHHHRHLEKRNVSQAOTDNTGISTSTAGKSGGDCSSMR-----ERR 959
 DB 1115 ESI-----SPGEDIDDDSERFKLLOQEFVYERE 1142
 QY 960 QSTASRHYDGSQOTPARPKYSSSHRNSSTNISTSQSELSNMCPSKSPVAVITPTAS 1019
 DB 1143 GNTDEDELEEDDLTA-----SKLTPEDESPAL-----TPPSP 1175
 QY 1020 DHRRTSMGSAKSNFVVSQSDLMWDTHTLSHA 1050
 DB 1176 FRDSVASGSSVPSS-PVSESVLCTPPNVTYA 1205

RESULT 9
 US-08-687-289A-8
 ; Sequence 8, Application US/08687289A
 ; Patent No. 5981195
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuller, Forrest H.
 ; APPLICANT: Krapcho, Karen J.
 ; APPLICANT: Hammerland, Lance G.

QY	639	FLAWETRVSPALNDSKHIGFVSNNVFITCLAGAAISLVISDRKDLVVF---	LLSPFII	69
Db	769	VIAIKTRGVP-ETENEAKPIGFTMTTCIVWLAFIPFGTSQADKLYIQTTTLTVSVS	82	
QY	696	FCTTATCLVFPKLVKRNPOGVVVKRVRA-----TLRPMK	74	
Db	828	LSASVSLGMLYMPKVYIILFHPQVPRKRSLKAVVTAATMSNKFOTKGNFRPNGEAKS	88	
QY	741	SVCE-LEQRLRDVKNT	755	
Db	888	ELCENLETPALATKOT	903	
RESULT				
US-08-823-110-1				
; Sequence 1, Application US/08823110				
; Patent No. 6077675				
; GENERAL INFORMATION:				
; APPLICANT: Stormann, Thomas M.				
; APPLICANT: Simin, Rachel T.				
; APPLICANT: Hammerland, Lance G.				
; APPLICANT: Fuller, Forrest H.				
; TITLE OF INVENTION: NOVEL HUMAN METABOTROPIC				
; TITLE OF INVENTION: GLUTAMATE RECEPTOR				
; NUMBER OF SEQUENCES: 16				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Lyon and Lyon				
; STREET: 633 West Fifth Street				
; STREET: Suite 4700				
; CITY: Los Angeles				
; STATE: California				
; COUNTRY: U.S.A.				
; ZIP: 90071-2066				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb				
; MEDIUM TYPE: storage				
; COMPUTER: IBM Compatible				
; OPERATING SYSTEM: IBM P.C. DOS 5.0				
; SOFTWARE: FastSeq for Windows 2.0				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/08/823,110				
; FILING DATE: March 24, 1997				
; CLASSIFICATION:				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: 08/604,298				
; FILING DATE: February 21, 1996				
; ATTORNEY/AGENT INFORMATION:				
; NAME: Wardburg, Richard J.				
; REGISTRATION NUMBER: 32,327				
; REFERENCE/DOCKET NUMBER: 224/259				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: (213) 489-1600				
; TELEFAX: (213) 955-0440				
; TELEX: 67-3510				
; INFORMATION FOR SEQ ID NO: 1:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 908 amino acids				
; TYPE: amino acid				
; STRANDEDNESS: single				
; TOPOLOGY: linear				
; MOLECULE TYPE: Peptide				
US-08-823-110-1				
Query Match 4.8%; Score 306.5; DB 3; Length 908;				
Best Local Similarity 20.8%; Pred. No. 1.9e-17;				
Matches 191; Conservative 158; Mismatches 350; Indels 219; Gaps				
QY	4	PSWFFASLLFLLWSTACGTAKR-----SDVVIAGFFP-YGDGVNSYTG----	49	
Db	12	PCFFLLTAKFWIL--TMMQRTSHQEAHSIRVDGDIILGLGFPVHAKRGVPCGKLUK	69	
QY	50	RGV--MPSVKLALGHVNEHGKILANYRLHWMNTOCN-----AAVGKSF	93	

D	b	357	VWFAEFWEENFGCKLGHGKRNHSHIKCTGLERIARDSYEQ-EGKVQFVIDAVYSMAYA	415
Q	y	339	IQQYVAERREDLLTHFDYRVKDWESV---FLEALRNTSPGVTG-PVRP-YNNERKANIL	392
D	b	416	LH---NMHKDLCPCYIGCLPRMSTIDGKELGYIRAVNPGSAGTPVFVNENGDPAGRYD	472
Q	y	393	INQFOL----GQMEKI GEYHSQSKHLDLS-----LG	419
D	b	473	IFQOITNKSTEYKVIGHWTNQ-LHLKVEDMQWAHREHTHPASVCSLCPCKGERKKTVKG	531
Q	y	420	KPVKW-----VGKTPPKDRP---LVIEHSQVNPTIYIVSASAS	455
D	b	532	VPCWCWHCEGEGNYQVELSCELCPLDQRPNNRNRTGCOLIPIKLEHSPMAVPVFEVA	591
Q	y	456	VIGVIIATVFLAFNIKYRNQRYIKMSSPHLNLIIVGCMITVLSIFIIGLDTLTSSAAAF	515
D	b	592	ILGIATTFVIIVFVRNDPPIVASGRESLSYVLGTGFICY-SITFLMI-----AAPD	644
Q	y	516	PYICTARAWILMAGFSFGAMSFKTWRVHSTFTDLKN---KKVKDYQLFMVWGVLILA	572
D	b	645	TIICSFRVFLGLCMCFSAALLTKTNHRIFIEQGCKSVTAPKFTISPASOLVITFSLIS	704
Q	y	573	IDIAIITTWIQADP-----PYRETQKLEPLUHHENIDDVLVIPENEYCQSEHWTFVSIYY	627
D	b	705	VQLLGVEFWFVVDPPHIIIDYGQRTIDP---EKARGVL-----KCDISDSLTCSL--	753
Q	y	628	AYKGLLVFGAFLAWETRHVSIPALNDSKHIGFSVNVFITCLAGAAISLVLSDRKLAVF	687
D	b	754	GYSILLMTCTVYANKTRGPV-ETFNEAKPIGFTMTTCIIWLAFIPIFFGTAQSAEKMY	812
Q	y	688	V---LLSFFFIFTCTALCVFPKIVELRNPGQGVDDRVR-----ATL-----	729
D	b	813	IQTTLTVMSLSLASVSLGMLYXPVYIIIFHFBEQNQVRKRKSRFNAVYTAATMQSKLIQK	872
Q	y	730	--RPMKNGKRRGROSSVCE-LEQRLRDVKNT	755
D	b	873	GNDRP---NGEVKSCELSETINTSTTKTT	899

RESULT 4
PCT-US91-09422-19
; Sequence 19, Application PC/TUS9109422
; GENERAL INFORMATION:
; APPLICANT: Mulvihill, Eileen R.
; APPLICANT: Hagen, Frederick S.
; APPLICANT: Houamed, Khaled M.
; APPLICANT: Almers, Wolhard
; TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09422
; FILING DATE: 19911212
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,007
; FILING DATE: 18-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/648,481
; FILING DATE: 30-JAN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/636,806

Matches 335; Conservative 156; Mismatches 300; Indels 169; Gaps 21;

QY 8 PFAILLFLLL-----WSTACGTAKRS-DVYTAGFPYGDGVNSVTGRGVM 53
Db 4 PPARLLLLLLPLLLPLAPGAWGARGAPRPPSPPLSLMGLMPLRKEVAKGSIGRGVL 63
QY 54 PSVKALGHVNEHGKILANRLHWNNDTCNAAVGVKSFDDMMHSGPNKVMFLFGAACTH 113
Db 64 PAVELAIEQRNE-SLLRPYFLDLRYDTECDNAKGLKAFYDAIKYGNHLMVFGGVCPS 122
QY 114 VTDPIAKASHWHLTOLSYADTHPMET-KDAFFNFFRVPSSENAFNAPRLALLKEFNWTR 172
Db 123 VTSIIAESLQGNVLQSPAATPVPLADKKKYPYFFRTVPSDNAVNPAILKLLKHQYOKR 182
QY 173 VGTYYQNEPRYSPLPHNMVADLAMEVEVVEVTFVNDVAESLKKLREKDVRIILGNFNE 232
Db 183 VGPLTQDQVRFSEVRNDLTGLVXGEDIEISDTESFSDNPDCTSVKLLKGNDRVRIILQFDQ 242
QY 233 HFARKAFCEAYKLDYGRAYQWLMATYSTDMWNVTDSECSVEEIALEAGAILVDLLP 292
Db 243 NMAAKVFC----- 250
QY 293 LSTSGDITVAGITADEYLVEYDRLR-GTEYSRFGHYTDGIWAAALAIQVY-----AEKR 346
Db 251 -----CTPOQYEREYNNKRSVGSFSGFHYAYDGIWIAKTLQRAMETLHASSR 299
QY 347 EDLLTHFDYRVKDWESVFLLEALRNTSFGVTPVRFYNNERKANILINQOLGOMEKIGE 406
Db 300 HQRIQDNFTDHTLGRILLNAMNETNFFGTQGVVFRNGERMGTIKFTQFQDSREVAVGE 359
QY 407 YHSQKSHLDLSLCKPKVWVGKTPPKORTLIYIEHSQVNPPIYIVSASVIGVITIAVFL 466
Db 360 YNAVADTLEI-INDTIRFQSEPPKDKTILEQLRKISLPLYSILSALTILGIMMASAFL 418
QY 467 AFNIKRYORYIKMSSPHLNNLIIVGCMITYLSIFIPLGLDTLSSVAAPFYICTARAWIL 526
Db 419 FFNIKRNQKLIKSSPYMNNLIILGMLSYASIFIFGLDGSFVSEKTFETLCTVTRWIL 478
QY 527 MAGFSLSFGAMFSGKTRVHSIFITDLKLNKKVIRKDYQLFMVGVVLLAIDIAITITWQADP 586
Db 479 TVGYTTAFGAMFAKTRVHAIFKNVKKMKKIIKDQKLLVIVGGMLLDLCILICWQAVDP 538
QY 587 FYR-ETKOLEPLHENID----DVLVIPENECYQSEHMTIFVSIYAYKGLLVFCGFL 640
Db 539 LRTVEKYSMEP-----DPAGRDISIRPLEHCENTHMTIWLGIYVAYKGLLMFLGCF 592
QY 641 AMETHRVSIPALNDSKHIGFSVYVFTTCLAGAAISLVLSDRXDLVFLVLSFFITFCTTA 700
Db 593 AMETHRVSIPALNDSKXIGMSVYVNGIMCIIGAASFLTRDQPNVQFCIVALVIFCSTI 652
QY 701 TLCLVFPKLVKLKRNPGQVY-DKRVRAIRLPMKSKNGRRDSSVCELEQ-----RLRDYKNT 755
Db 653 TLCLVFPKLVKLITLRTNPDAATQNRREQFTQNKKEDSKTSTSVTSVNAQSTSRLEGQSE 712
QY 756 NCRFRKALMEKENELQALIRKL--GPEARKWIDGVCTGGSNVGSELEPILNDDIVRLSA 813
Db 713 NHRLRMKITELDKLEVTMOLQDTPEKTYIK-----QNHQYQELNDILN----- 757
QY 814 PPVREMPSTVTTEM-TSVDSVTSTHVEDMNSFVSQSTVMAPSLPKKKQKQSVIEHSH 872
Db 758 -----LGNFTSTDGKAILKLNHLDQN-----POL-----QNTT 787
QY 873 APAPTMQPIQO-QLOAHLQHQHQOQOHLQOQOHOQOQOQOQOHHHRLHLEKRNVSVA 931
Db 788 EFSRTCKDPEDINSPEHIQRRLSLQIPIL-----HHAYLPSIGGVA 830

RESULT 2

US-09-183-253-4

; Sequence 4, Application US/09183253

; Patent No. 6043054

; GENERAL INFORMATION:

; APPLICANT: VAWTER, LISA

RESULT 3

US-08-855-146-2

APPLICANT: STAMMERS, MELANIE
TITLE OF INVENTION: NOVEL COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,253
FILING DATE: 30-OCT-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9817907.0
FILING DATE: 17-AUG-1998
APPLICATION NUMBER: 60/075,306
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70395
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-253-4

Query Match 12.08; Score 768; DB 3; Length 332;

Best Local Similarity 46.6%; Pred. No. 4e-58;

Matches 151; Conservative 67; Mismatches 92; Indels 14; Gaps 5;

QY 353 FDIRVKDWESVFLBALRNTSFEVTPGVRFYNNERKANILINQOLGOMEKIGEVHSOKS 412

Db 5 FNYTDHTLGRILLNAMNETNFFGTQGVVFRNGERMGTIKFTQFQDSREVAVGEYNAVD 64

QY 413 HLDLSLCKPKVWVGKTPPKORTLIYIEHSQVNPITYIVSASVIGVITIAVFLAFNIKY 472

Db 65 TLEI-INDTIRFQSEPPKDKTILEQLRKISLPLYSILSALTILGIMMASAFLFFNKN 123

QY 473 RNQYIKMSSPHLNNLIIVGCMITYLSIFIPLGLDTLSSVAAPFYICTARAWILMAGFSL 532

Db 124 RNQLIKMSPPYNNLIILGMLSYASIFLFLDGSFVSEKTFETLCTVTRWILTGYTT 183

QY 533 SFGAMFSGKTRVHSIFITDLKLNKKVIRKDYQLFMVGVVLLAIDIAITITWQADPFYR--E 590

Db 184 AFGAMFAKTRVHAIFKNVKKMKKIIKDQKLLVIVGGMLLDLCILICWQAVDPLRRTVE 243

QY 591 TKOLEPLHENID----DVLVIPENECYQSEHMTIFVSIYAYKGLLVFCGFLAWETR 646

Db 244 KYSNEP-----DPAGRDISIRPLEHCENTHMTIWLGIYVAYKGLLMFLFCFLAWETR 297

QY 647 VSIPLNDSKHIGFSVYVNV-FITC 669

Db 298 VSIPLNDSKYIGMSVYVNGIISC 321

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OM protein - protein search, using sw model

Run on: April 30, 2002, 09:52:02 ; Search time 26.74 Seconds
(without alignments)
1026.702 Million cell updates/sec

Title: US-09-715-962-4
Perfect score: 6409
Sequence: 1 MFRPSWFFASLLFLLWST.....SAVGQSCPNIKCDIVEYL 1220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1442.5	22.5	859	US-09-183-253-2	Sequence 2, Appli
2	768	12.0	332	US-09-183-253-4	Sequence 4, Appli
3	311	4.9	908	US-08-855-146-2	Sequence 2, Appli
4	309	4.8	912	PCT-US91-09422-19	Sequence 19, Appli
5	306.5	4.8	908	US-08-823-110-1	Sequence 1, Appli
6	306.5	4.8	908	US-08-604-298-1	Sequence 1, Appli
7	305	4.8	912	US-08-617-785-2	Sequence 2, Appli
8	297	4.6	1219	US-08-687-289A-6	Sequence 6, Appli
9	295.5	4.6	1056	US-08-687-289A-8	Sequence 8, Appli
10	290.5	4.5	922	US-08-617-785-14	Sequence 14, Appli
11	286.5	4.5	915	US-08-617-785-12	Sequence 12, Appli
12	285.5	4.5	1056	US-08-687-289A-7	Sequence 7, Appli
13	281	4.4	867	US-08-617-785-4	Sequence 4, Appli
14	280.5	4.4	915	US-08-453-862-2	Sequence 2, Appli
15	280.5	4.4	915	US-08-452-734A-2	Sequence 2, Appli
16	280.5	4.4	915	US-08-176-401B-2	Sequence 2, Appli
17	280.5	4.4	915	PCT-US94-14989-2	Sequence 2, Appli
18	278.5	4.3	1212	US-08-660-148-5	Sequence 5, Appli
19	277	4.3	877	US-09-128-280-2	Sequence 2, Appli
20	276.5	4.3	1194	US-08-538-526-1	Sequence 1, Appli
21	268	4.2	877	US-08-407-875-2	Sequence 2, Appli
22	267.5	4.2	1180	US-08-660-148-2	Sequence 2, Appli
23	266.5	4.2	1212	US-08-486-270-10	Sequence 10, Appli
24	266.5	4.2	1212	US-08-367-264-10	Sequence 10, Appli
25	265.5	4.1	1079	US-08-485-588-8	Sequence 8, Appli
26	265.5	4.1	1079	US-08-484-565-8	Sequence 8, Appli
27	265.5	4.1	1079	US-08-480-751-8	Sequence 8, Appli

28	265.5	4.1	1079	2	US-08-943-986-8	Sequence 8, Appli
29	265.5	4.1	1079	3	US-08-353-784-8	Sequence 8, Appli
30	265.5	4.1	1079	3	US-08-484-719B-8	Sequence 8, Appli
31	264.5	4.1	1212	1	US-08-072-574-10	Sequence 10, Appli
32	261.5	4.1	1199	1	US-08-041-538-2	Sequence 2, Appli
33	261.5	4.1	1199	1	US-08-463-642-2	Sequence 2, Appli
34	261.5	4.1	1199	1	US-08-455-602-2	Sequence 2, Appli
35	261.5	4.1	1199	1	US-08-465-157-2	Sequence 2, Appli
36	261.5	4.1	1199	5	PCT-US91-09422-2	Sequence 2, Appli
37	258	4.0	905	1	US-08-072-574-2	Sequence 2, Appli
38	255.5	4.0	1180	1	US-08-486-270-8	Sequence 8, Appli
39	255.5	4.0	1180	3	US-08-367-264-8	Sequence 8, Appli
40	254.5	4.0	906	1	US-08-486-270-2	Sequence 2, Appli
41	254.5	4.0	906	3	US-08-367-264-2	Sequence 2, Appli
42	252.5	3.9	1180	1	US-08-072-574-8	Sequence 8, Appli
43	250.5	3.9	906	5	PCT-US91-09422-17	Sequence 17, Appli
44	249	3.9	1078	1	US-08-485-588-7	Sequence 7, Appli
45	249	3.9	1078	1	US-08-484-565-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-183-253-2
; Sequence 2, Application US/09183253
; Patent No. 6043054
; GENERAL INFORMATION:
; APPLICANT: VAWTER, LISA
; APPLICANT: STAMMERS, MELANIE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09183,253
; FILING DATE: 30-OCT-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9817907.0
; FILING DATE: 17-AUG-1998
; APPLICATION NUMBER: 60/075,306
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70395
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-183-253-2

Query Match 22.5%; Score 1442.5; DB 3; Length 859;
Best Local Similarity 34.9%; Pred. No. 9e-116;

Db 785 FLIGYTCLLAAICFFFAKSR--KLPENFNEAKFITFSMLIFFIWIWISFIPAYASTYGF 842
QY 675 ISLVLSDRKDLVFLLSRFIIFCTTATLCLVFPKLVKLKRNPOGVVDK----- 723
Db 843 VSAV-----EVJAILAASFGLLA-----CFFNKIYIILFKPSRNTIEEVRCSAAHAFK 892
QY 724 -RVRA TLPRMSKNGRRSDSVCLEQRLRDVKNTNCRFKALMEKENELQALIRKLGPEAR 782
Db 893 VAARATLRNSVSRKSSSL----- 912
QY 783 KWIDGVTCTGGSNVGSELEPIILNDDIVRLSAPPVRRMPSTTVMSTSVSTHVM 842
Db 913 -----GGSTGS-----TPSSSISS----- 926
QY 843 NSFVSVQSTVMAPSLPPKKKQSIVEHHISHAPATMMQPIQOOLQOHL---QQHQOQOQ 899
Db 927 -----KNSDEPFP---RPERKQOQPLALTQOEOQOQOPL 958
QY 900 HLOQOQHOQMO-----QQOQOQOHHHRHLEKRNVSVAQTDNIGS 939
Db 959 TLPOOORSQQPRCKOKVIFGSGVTFTSLSFDEPOKNMAHRNSTHONSLEAO----- 1011
QY 940 ITSTAGKRSGDCSSMRERROSTASRH-----YDSGSQTPTA---RPK 979
Db 1012 -----KSSDTLTHQPLPLQCGETDLDLTQVETGLQGPVGGDORPE 1053
QY 980 YSSSHRNS-STNISTSQS 996
Db 1054 VEDPEELSPALWVSSQS 1071

Search completed: April 30, 2002, 10:06:10
Job time: 378 sec

ionotropic glutamate receptor homolog GLR4 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C:Accession: F51137
R:Davenport, R.J.; Kiegle, E.A.; Tester, M.
submitted to the EMBL Data Library, September 1999
A:Description: Cloning of an ionotropic glutamate receptor homolog from Arab
A:Reference number: Z25310
A:Accession: F51137
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-976 <DAV>
A:Cross-references: EMBL:AF189332; PIDN:AAF01294.1
C:Genetics:
A:Gene: GLR4

Query Match 3.9%; Score 248.5; DB 2; Length 976;
Best Local Similarity 18.8%; Pred. NO. 5e-07;
Matches 117; Conservative 99; Mismatches 252; Indels 153; Gaps 22;

Qy	25	TAKRSDVYIAGFPYDGVNSYTGKVPMSVKLAGHVNHGKILANYRLHMMWNDQC	84
Db	44	TORPSSNVNGALETY-----DSFIGNAAKPAVKAAMDNDVNDQTVLKGKILNFIQDSNC	98
Qy	85	NAAVGVKSFDDMHSGPNKYM-LFGAACTHVTDPKAKSKHWHLTOLSYADTHPMTKDA	143
Db	99	SGFIGMGALQJME--NKVVAIGPOSSGIAHMI SVANELHVPPLSGATDPTLUSSIQ	155
Qy	144	FPNFFRVVPSSEAFNAPRLA-LIKEFNWTRGVGVYQNEP--RYSLPHNHMVAIDLADAMEYE	200
Db	156	FPYFLRTRTQND-YQMHAIADEFLSYSGWRQVIAIFVDDCEGRNGI---SVLSVDLAKKRS	211
Qy	201	VVEQTQSFVNDVAES-----LKKLREKDVRIILGNFNEHFARKAFCEAYKLDMYGRAYOW	254
Db	212	RISYKAAITSGADSSITRDLVSVNLMESKRVFVHVHVPDGLNVFSAKSLGMMASGYW	271
Qy	255	LIMATYSTDMWNTQDSECSVE-EIATALEGAILVDLLPLSTSGDITVAGITADEYLVEY	313
Db	272	I-----ATDMLPTAMDSMEHVDSDTMDLQGVV-----AFRHYTIESSVKRQFMAW	318
Qy	314	DLRLGTE-YSRFGHYTVDGIWAALAIIQYVAEKREDL-----LTH	352
Qy	319	KNLRPNDFGNSIYAMAYDSVLMVARALDVPFRENNTITESNDPNLHKTNGSTIQLSALS	378
Qy	353	FDYRVKDWESVFLEALRNTSFEGTGPVPRVYNNERKANILINQOL-QGMEKIGEVHSOK	411
Db	379	FNECEK-----FMKILGMHMTGTGPIQIDSDRNRVNPAYEVNLLEGATPRVTGVWSNH	433
Qy	412	SHLDL-----SLGKPKVWVG-----426	
Db	434	SGLSVHPHETLYSRPNTSTANQRLKGIYPGEVTKPPRGWFPNKGKPLR-IGVPNRVS	492
Qy	427	-----KTP-----PKDRTLIYIEHSQVNPTI--YIVSASASV	456
Qy	493	YTDVVKDKNPPGGVGYCIDVFEAAIELLPYPPRTYILYGDGRKNRPSYDNLVNEVVADN	552
Db	457	IGVIIATVFLAFNIKRYNRQYIKMSSPHLNLIIVGCMITYLSIIFLGLDTTLLSSVAAPP	516
Db	553	FDVAVGDIITVN---RTRYVDFTQPFIESGLVVVAPV-----KEAKSSPWSFL	598
Qy	517	YICTARAWILMAGESLSFGAM	537
Db	599	KPFTIEMWAVTGGFFLEVGAM	619

RESULT 15

calcium receptor (clone phpCar-5.2) - human
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: B56715
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.

J. Biol. Chem. 270, 12919-12925, 1995

A:Title: Molecular cloning and functional expression of human parathyroid calcium receptor

A:Reference number: A56715; MUID:95279439

A:Accession: B56715

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1088 <GAR>

A:Cross-references: GB:U20760; NID:g683746; PIDN:AAA86504.1; PID:g683747

C:Keywords: glycoprotein; receptor; transmembrane protein

Query Match 3.9%; Score 247; DB 2; Length 1088;
Best Local Similarity 17.4%; Pred. No. 7.2e-07;
Matches 223; Conservative 177; Mismatches 370; Indels 508; Gaps 56;

Qy	12	LLFLLLLSTAC----	GRtakRsdvY	IAgFFpYgDgVENS-	----	YtGRGv	52
Db	9	VLLALtWHTSAYGpDQRAQKKGdILlGGFLpIHfGvAAKQDdLKSrPESvECIRYnRGf	68				
Qy	53	--MPsvKlALGHvNEHGKILANyELHmWwNDtOCNA-----				AVGVKS	92
Db	69	RwLQAMlFAIDeINSSpALLpNLtLgRYIdFT--CNtVSKALEATLsfvAQNkIDSLNdLE	127				
Qy	93	FFdMMHGSPKvMFLGAACTHvTDIAKAKSHWHLtOLsYADThPMFT--KDAPpNFRvV	151				
Db	128	FCNCSEHlPSTlAVVGATGSGvSTAVANLLGLFIPQvSYASSRLLSNKQFKSLRlT	187				
Qy	152	PSENAFNAPRLALKEFNwTRvGTvYONePRYSLPH-----	187				
Db	188	PNdEHQATAMADlTEYFRvNMWvGTlAADDD--YGRPGIEKfREAEERDlCIDfSELISoY	246				
Qy	188	-----NHwADLdAMEvEVvETQsfvNDvAESlKLlREKdV-----	223				
Db	247	SDEEIQuIVEvIOnSTAKvIvFvSSGpDLlELIKElVRNlTCKlWlASEAWASSLlA	306				
Qy	224	-----RIILGNfNEHFARKA-----	FCeAYKlDMYGRAYOWlIMATYsTDWNvTODS	273			
Db	307	MPQYfHVvGGTlG--FALKAGQlPGfREFLK--KVHPRK----	SVHNGfAKEfWEET--FNC	358			
Qy	274	SVEElATALECAIlVDLL-----	PLSTSGDlTVAGlTAdEYlVEYD	314			
Db	359	HLQEGa----KGpLpVDfLlRGHEESGRfSNSfAFRPlCT--GdENIssV--ETPyIdT	412				
Qy	315	RLRGTEYSRPhGYTDGwIAAAlAQ--YvAEKREDLlThFD----	YRVKdWESvFLEAl	368			
Db	413	HLR--ISYN-----	vYLAVYSTAHAlQDIYtCLpGRGLfTNGSCADlKKvEAMQ--VLKHL	464			
Qy	369	RNTsfEGVTG-----	PVRfYN-----	N	385		
Db	465	RHLNfTNMGEGvTfDECGDLvNGYSIInWHLSPEDGSIVfKEvGYvNYvAKKGERlFN	524				
Qy	386	ERKANIlINQfQ-----	lQOMEKI-----	GE	406		
Db	525	EEK--IlWSGfSREPlTFvLSVLvQPFvSNCsROClAGTKRGIlTEGPtCCfECvCPdGE	582				
Qy	407	YH-----	SOKSHLDslGpKvWVGtTPPKDRtlVlEHsQvNpTYiV	450			
Db	583	YSDETdSACNKCPDDfWSNENHTS--ClAEIEfLSWTEfFGAl-----	TlF--	529			
Qy	451	SASASvIGvIATvELAFNATKYNORvYKMSpHLNlIvGCMTY--lSIlFLGLDtlTL	509				
Db	630	---AVLGIflTAFvLGvFikFRNTPiVKATNRelsYLLfSLlCCfSSlLFFlG-----	680				
Qy	510	SSvAAFPYlCTARAWlMAGfSLSGfAMfSKTRvHvSHlFTDLKlNKvIKDY-----	QlPM	565			
Db	681	---EPQDWTCRLRQPAFGISvLCISlLVKTRvLLVf--EAKlPTsFhRKWGLNlQlFL	736				
Qy	566	VvGLlADlAlITw--QlADpFYRETKQLEPlLHENIdDVLvPENeYCOSEHMTlFvS	624				
Db	737	LVfICTfMQIVlCVlWlYtAPPSSYRQOELE-----	DElIfT-----	CH--EGSLMAlG	784		
Qy	625	lIYAKGLlLLvFGAlAWETRHvSlPA--LNdSKHlGfSVNYvNfTlClA-----	GAA	574			

QY 331 GIWAAALAIQYV-----AEKREDLLTHFDYRVKDWESVFLAALNTSFEQVT 377
 Db 401 AVYIAHALHSMHQALCPGHTGLCPAMEPTDGRTHLHY-----IRAVRFNGSA 448
 QY 378 G-PVRF-YNNERKANILINQFOL-----GOMEKIGEYHSQSHLDLSLGKPKVKGW-- 426
 Db 449 GTPVMEENGDAFCRYDIQYQATNGSSASSGGYQAVQGW-AEALRLDMEV---LRWSGDP 504
 QY 427 -KTTPKDRTL-----IYIE-----HSQ 442
 Db 505 HEVPPSQSLPCGPGERKKMKVGPCCWHCEACDGYRFQVDEFTCEACPGDMRPTNHTG 564
 QY 443 VNPTIYI-----VNSASVIGVVIATVFLAFNIKYRNQRYIKMSSPHLNLIIVG 492
 Db 565 CRPTPVRLTWSSPWAALPLLALGIMATTTINATFMRRNDTPIVRASGRELSYVLITG 624
 QY 493 CMITYLSIIFLGDDTTLSVVAAPP--YICTARAWILMAGFSLGFSKFTWRVHSIFTD 550
 Db 625 IFLIY-AITFL-----WAEPCAAICARRLLGLGTLTYSALLTNTNRIYRFEQ 675
 QY 551 LKLNKK-----VIKDYQLFMVVGVLAIADIAITTTQIADP-----FYRETQKLEPLHEN 601
 Db 676 GKRSVTPPPFISPTSLVITFG-LTSLQVVGVIATLGAQPPHSDVIDYEQRTVDP---EQ 731
 QY 602 IDDLVIVPENECQSEHMTIFVSIYAYKGLLVFGAFLAWETHRVHSIPALNDSKHIGFS 661
 Db 732 ARGVL-----KCDMSDLISLIGL--GYSLLMVTCTVYAIKARGVP-ETFNKAPICGT 782
 QY 662 VYNVEITCLAGAAISLVLSRDKDLVFN---LLSFFIIFCTTATLCLVFPKLVKLKRNQ 718
 Db 783 MYTTCIINLAFVPIFGTAQSAEKIYIQTTLTVSLSASVSLGMLYVPRKYVILFHP 842
 QY 719 GVYDKRVRATLR-----PMSKN 735
 Db 843 QNVQKKRSLKKTSTMAAPQONEN 866
 RESULT 12
 A42916
 C:Species: rattus norvegicus (Norway rat)
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C:Accession: A42916
 J. Biol. Chem. 267, 13361-13368, 1992
 A:Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5
 A:Reference number: A42916; MUID:92317054
 A:Accession: A42916
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1171 <ABE>
 A:Cross-references: GB:D10891; PID:g220813; PID:BAA01711.1; PID:d1002186; PID:g220814
 A:Experimental source: brain
 A>Note: sequence extracted from NCBI backbone (NCBI:107749, NCBI:107750)
 C:Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 4.0%; Score 256; DB 2; Length 1171;
 Best Local Similarity 18.9%; Pred. No. 2.3e-07;
 Matches 225; Conservative 154; Mismatches 381; Indels 428; Gaps 52;
 QY 60 LGHVNHEGKILANRYLHMWNNDTQCNAAGVGVKSPFDMN----- 97
 Db 76 LERINDPTLLPNITLCCEIRDSCHWSAVALAQESIEFIRDSLSISSEEEGLVRCVDSGS 135
 QY 98 -HSGPNKVMFLFGAACTHTVDPIAKASHWHLTQLSYADTH-PMFTKDAFNFFRVVPSN 155
 Db 136 FRSKKPIGVIGPGSSVAIQVQNLQLFNIPQIAYSATSMDLSLDTLKFYFMRVWPSDA 195
 QY 156 AFNAPRLALLKEFNWTRVGVYQNEPRYSPLPHNMWADLDAME-VEVVEYQSFVNDVAES 214
 Db 196 QQARAMVDIVKRYNWTYVSVAHV-TEGNYGESGMEAFKDMSAKEGICIAHYSKIYSNAGEQ 254

RESULT 13

A56715

calcium receptor (clone phpCar-4.0) - human

C:Species: Homo sapiens (man)

QY 215 -----LKKLRE--KDVRIILGNFNEHFARKAFCEAYKLDMYGRAYQWOLIMATYSTDMWNV 267
 Db 255 SFDKLLKKLRSHLPKRVV-----ACFCE-----GMTVRGLMA----- 288
 QY 268 TDSECSVEEIIATALEGAILVDLLPLSTSG-----DIT-----VAGITA----- 306
 Db 289 -----MRLGLAGE-----FLLGSDGWADRYDVTGQREAVGGITIKLQSPDKW 335
 QY 307 -DEYLVEYD-----RLRG--TEYSRFE----- 325
 Db 336 FDDYVYKLRLPETNLNRPWFQEFWQHRCLEFAGFAQENSKYKNTCNSSITLTHHVQDSK 395
 QY 326 -GYTYDGIWAAALAIQYVAEK-----RELLTHFDYRVKDWESVFLAALNTSFEQVT 377
 Db 396 MGFVINATYSMAYGLHNMOMSLCPGYAGLIDAMKPIDGR-----KLDSLAKNTFTGVS 449
 QY 378 GPVRFY--NNERKANILINQFOLGOMER-----IG-----EYHSQSHLDL 416
 Db 450 GDMILFDENGOSPGRYEIMNFK--EMGRDYFDYINVGSNDGELKMDDEWVSKNNIIR 507
 QY 417 SL-GKP-----VKWYVK-----TPPKDRTLIYIEHS----- 441
 Db 508 SVCSEPCGKQIKVIRKGEVSCCWTCTPCKENEYVDFEYTKACQLGSWPTDGLTCCDLI 567
 QY 442 -----QVNPTIYVSASVIGVVIATVFLAFNIKYRNQRYIKMSSPHLNLIIVG- 492
 Db 568 PVQYLRWGDPEPIAAVFAFLGLLATLFTVTF--LIYRTPVVKSSRELICYILAGI 624
 QY 493 -----CMIT-----YLSIIFLGDDTTLSVVAAPPYICTARAWILMAGFSLSGAM 537
 Db 625 CLGYLCTFLIAKPKQIYCYLQIGIGLSP-----AMSYAL 661
 QY 538 FSKTWRVHSIETDLKLNKKVTKDYQLFM-----VGVLLAIDIAITTTQIADPFPYRE 590
 Db 662 VTKNRIARILAGSK--KKICTKKPRFMSACAQLVIAFLICIGIIVAIIMEP---- 715
 QY 591 TKQLEPLH-HENIDDLVIVPENECQSEHMTIFVSIYAYKGLLVFGAFLAWETHRVHSI 649
 Db 716 --PDIMHDYPSIREVYLI-----CNTTNLGVVTP--GYNGLLILSCTFYAFKTRNV-- 763
 QY 650 PA-LNDSKHIGFSVYVNVITCLAGAAISLVLSRDKDLVFLVLSFFIICTTATLCLVFP 708
 Db 764 PANFNEAKYIAFTMYTTCIINLAFVPIYF--GSNYKIITMCFVSLSATVALGCMFVP 819
 QY 709 KLVELKRNPGQVVDKVRATLR-----PMSKNGRDSSVCELEOR----- 748
 Db 820 KVIILAKP-----ENVRSAFTTIVVRHVHVDGKSSSAARSSSLVNLNKRSGSGETL 875
 QY 749 -----LRDVKNNTN-----CFRKLMEKENELQ-ALIRKLGPEARKWIDGVCTGG 793
 Db 876 SNGKSVTWAOQNEKSTRGOHLWQRLSVHINKKENPNQTAVIKPPFKSTENRGPAAAGGG 935
 QY 794 SNVSGSEPIILNDDIVRLSAPPVRREMSTVTEMTSVDSVTSTHVEDMNSFVSQSVTM 853
 Db 936 SGPG--VAGAGNAGCATATGPG---EPPDAGPKALYDV-----AEAESEFPA----- 976
 QY 854 APSLPKKKKQSIIVEHSHAPATWMOPTQQOQLQHQHQOQHQOQHQOQHQOQ 913
 Db 977 -----AARPSPSLIST----- 988
 QY 914 QQQHHHRLHLEKRNVSQAOTDDNIGSITSTAGKRSGGDCSSMRERRQSTASRHYDSGOT 973
 Db 989 -----LSHLACSAGRTDDAPSLHSETAARSSSGSLMEQISSLVVTRF----- 1032
 QY 974 PTARPKYSSHRNSTNTISTQSELSNMCNCPKSPKTPAVIKTPTASDH 1021
 Db 1033 -----TANI-----SELNSNM-LSTAATPGPGTPICSSY 1061

QY 23 GRTAKRS-----DVIYAGFP-----PYGDGVENSYTCR-----CV--MPSVKLALGHVN 64
Db 31 GASSQVARMGDVVIIGALFSVHHQPPAEKPERKCGEIRQYQIQVEMFHTLDKIN 90
QY 65 EHGKILANRLHMMWNTQCNAAVGVKSFDDMMH-----SGPNKVM----- 105
Db 91 ADPVLNITLGSIRDSCHWSSVALQSIIEFIRDSLISIRDEKDLNRCPLPDGOTLPPG 150
QY 106 -----LFGAACHTHVTDPIAKASKHWHLQLSYADPH--PMFTKDAFPNFFRVVPSNA 156
Db 151 RTKPIAGVIGPGSSVAIQVONLLQLFDIPQIAYSATSIDLSTKLYKYELRVVPSDTL 210
QY 157 FNAPLALLKEFNWTRVGTVYQNEPRVSLPHNHVADLDAME--VEVETQSFVNDVAES- 214
Db 211 QARAMLDIVRYNNYTVYSAVH--TEGNTGESGMDAFKELAAQOGLCIAHSKDIYSNAGEKS 269
QY 215 ----LKLREK--DVRILGNFNEHFARKAFCEAY-----KLDYGRAYQWLIWA 258
Db 270 FDLRLKRLRPLKRVV-----CFCBGTVRGLLSAMRRLGVGGE-----FS 313
QY 259 TYSTDWNNVTQDSECSVEEITALEGAILVDL-----LPLSTSGDITVAGI 304
Db 314 LIGSDGN---ADRDVEIEGVEVEANGGITIKLQSPVRSFDDYFLKLRDLTN----- 362
QY 305 TADYLYVEY-----DLRG--TEYSRPH-----GYTDGIWAAL 337
Db 363 TRNPFPEFWQHRFQCRPLGHLLENPNFKVCTGNESLEENYVODSKMGFVINAIYAMAH 422
QY 338 AIOVV-----AEKREDLLTHFDYRVKDWESVFLEALRNTSEFEGVTGPVRFPYN 384
Db 423 GLQNMHALCPGHVGLCDAMKPIDGRKLLDFLIK-----SSFVGVSGEEWFD 470
QY 385 NERKA-----NLINQFOLGOMEKIEYHSQKSHLD---LSLKG----- 420
Db 471 EKGDPAGRYDIMNLYQTEANRYDVHVGTWHEGVLINIDDIYKIQNMKSGMVRVSCPECLK 530
QY 421 -PVKWGK-----TPPKDRPLI-----YIEHSQ 442
Db 531 GOIKVIRKGEVSCOWICTACKENEFVODEFTCRACDLGWNPAELTGCEPIPVRYLENSD 590
QY 443 VNPTIYIVSASVIGVITVFLAFNFKIKYRNQYIKMSSPHLNNLIIVGCMITVLSIF 502
Db 591 IES---IIATFSCGLIVLFLVFLVLYRDTVPVKSSRELVCYIIAG-----IF 639
QY 503 LGLDTLSSVAAFPYIC-----TARAWI--LMAGFS--LSFGAMFSKTRVHSIFT 549
Db 640 LG-----YVCPFTLIAKPTTSCVYLQRLVGLSSAMCYSAVLTXTNRIARILA 687
QY 550 DLKLNKVIKDYQLFM-----VGVLLAIDIAIITWQIADFPYRTKOLEPLHHENI 602
Db 688 GSK--KKICTRKPFRMSAWAQVIIASILISVQLTLVTLIIMEP-----PMPILSYPSI 739
QY 603 DDVLIVIPENEYCOSEHMTIFVSIYAYKGLLVFGAFLAWETRHSIPA--LNDSKHIGFS 661
Db 740 KEVTLI-----CNFSNGLVWAPV--GYNGLLIMSCITYAFKTRNV--PANENAKYIATF 790
QY 662 VYNVFTCLAGAAISLVSOKDLVFLVLLSPFIIFCTATLCLVFPVKLVBKRNPGQW 721
Db 791 MYTTCIILWAFVPIYF---GSNKIITTCFAVLSVTVAGCMFTPKMYIILIAKP----- 842
QY 722 DKRVRAFL-----RPMKNGRRD--SSVCELEQRURD 751
Db 843 ERNVSAFTTSDVVRMHVGDGKLPSCRNTFLNIPRRKKPGAGNANSNGKSVSWSEPGGRQ 902
QY 752 V-NTNCRFRKALMEKENEL-----QALIRKLGPEARKWIDVGTCTGS-----NVGSE-- 799
Db 903 APRGQHWQRLSVHVKTNACNOTAVIKPLTKSYOGSGKSLTFSADSTKTLYNVEEDN 962
QY 800 -----LEPILNDDIVRLSAPPVRRMPTVTTVEMTSVDVSTVTHVENDSNFSVQSIVM 853
Db 963 TPSAHFPPSPSPSMVVRHRRGPPVATTP-----LPPLHTAEETPLFLADSVI 1009
QY 854 APSLPPKKKKQKQIVHEHSHAPATMMQPIQO--QLQOHLQ----- 891

Db 1010 PKGLPPLPQQ-----OPQPPPPQPPQPKSLMDQLQGVVTFNGSGIPDFHAVLAGP 1062
QY 892 -----HQOQQOQHLOQQOQHQQOQQOQQOQQOHHHLEKRNVSVAQTD 934
Db 1063 GTPGNSLRSLYPPPPPPQHQLMLPLHLSTFQESI----- 1097
QY 935 DNIGSITSTAGKRSKSGDCSSMR-----ERQOSTASRHYDSGSGTPTTARPKYSSSHRNS 987
Db 1098 -----SPPGEDIDDDSERFKLQOEFVYREBGTTEDELEEEEDLPTA----- 1139
QY 988 STNISTSQSELNMCPSHSPKSPYAVIKTPTASDHRTSMGSKNSFNVSQSLMDWTHL 1047
Db 1140 -----SKLTPEDSPAL-----TPSPFRDSVASGSSVPSS--PVSESVLCTPPNV 1182
QY 1048 SHA 1050
Db 1183 TYA 1185
RESULT 11
A46742
metabotropic glutamate receptor, mGluR6 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A46742
J. Biol. Chem. 268, 11868-11873, 1993
A:Title: Molecular characterization of a novel retinal metabotropic glutamate recepto
A:Reference number: A46742; MUID:93280152
A:Accession: A46742
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-871 <NAK>
A:Cross-references: GB:D133963; NID:g391856; PIDN:BAA03066.1; PID:g391857
A:Experimental source: retina
A:Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBIP:133250)
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; transmembrane protein
Query Match 4.0%; Score 258.5; DB 2; Length 871;
Best Local Similarity 19.9%; Pred. No. 1.1e-07;
Matches 184; Conservative 154; Mismatches 321; Indels 265; Gaps 44;
QY 12 LFLFLW-----STACGRTAKR--SDVYIAGFP--YGDGVENSYTG-----RGV--MPSVK 57
Db 8 LLWLAWLSQAGIACAGSVRLAGGLTIGGLFPVHARGAAGRACGALKKEQGVHREAML 67
QY 58 LALGHVNEHGKILANYRLHMMWNTQCN-----AAVGVKS 92
Db 68 VALDRVNADPELLGVRLGARLLDT--CSRDTVALEQALSFVQALINGRGGDEASVRCPG 126
QY 93 FDMHSGPNK--VMLFGAACHTHVTDPIAKASKHWHLQLSYADTHPMETKDAFPNFF-R 149
Db 127 GVPPLRSAPPVRVAVGVASASSIMVANVRLFAIPQISYASTAPELSDSTDFFSR 186
QY 150 VVPSNAFNAPRLAILKENFTWTRVGTVYQNEPRVSLPHNHVADLDAMEVEVETQSFVN 209
Db 187 VVPPDSYQAQAMVDIVRALGWNVSTL-----ASEGNYGSGVEAF--VQISRAGGV- 237
QY 210 DVAESLKLRE-----KDVRIILGNFNEHFARKAFCEAYKLDYMTGRAYQ 253
Db 238 CIAQSIKIPREPKEPFHKVIRRLMETPNARGLIIFANEDDIRRVLEATRQANLGH-FL 296
QY 254 WLIMATYSTDWNNVTQDSECSVEEITALEGAILVDLP----- 292
Db 297 WY-----GSDSWGSKISPIINLEEEAV---GAITI--LPKRASIDGFDQYFMTSRLENNR 346
QY 293 -----LSTSG---DITVAGITADEYLVE---YDLRGTEYSRFGHYTD 330
Db 347 RNINWFAEFEEFNCKLTSSGQSDSTKRCTGEIRIGDSAYEQEGKVQ-----FVID 400


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QY 765 EKENEALIRK--LGPEARKWIDGVTCTGGSNVSELEPIILNDDI-----VRLSAPP 815
Db 885 QHKSEIECFTPKGSMG-----NGGRATMSSNSKSVTWQNEKSSRGQHLWGLSLIHI 937
QY 816 VRRPMPSTTTVTEMTSDVSTSHV-----EMDNSFVSQSTYMA-----PSLPP--K 860
Db 938 NKKENPNOTAVIKFPFKSTESRGLCPGRGAGSAGGVATGGAGCAGAGPGPESPADGP 997
QY 861 KKKOSIVVEHHSHAPAPMMQ---PIQQOOLQHLQHOQHOQOOLQHOQOHOQOQOQO 917
Db 998 KALYDVAEAEHEHPAPAPRSPSIST-----1024
QY 918 HHRHLEKRNVSQAQTDNIGISITAGKRGSGDCSSMRERROSTASRHYDSGQTPPTAR 977
Db 1025 -----LSHRAGASRTDDVPSLHSEVPARSSSGSLMEQISSVVTRP-----1068
QY 978 PKYSSSHRNSTNISTSOSELSNMCPSKPTPAVIKPTASDHRRTSMGSAKSNFVV 1036
Db 1069 -----TANI-----SELNSMMLSTAAPSPGV-----GAPLCSYLI 1099

RESULT 8
Metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: J02132
R:Nakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: J02131; MUID:94197696
A:Accession: J02132
A:Molecule type: mRNA
A:Residues: 1-1180 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
F:580-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>

Query Match 4.28; Score 270.5; DB 2; Length 1180;
Best Local Similarity 19.38; Pred. No. 3.1e-08;
Matches 221; Conservative 145; Mismatches 343; Indels 439; Gaps 52;
QY 104 VMLPGAACHTVDPIAKSKHWHLTQLSYADTH-PMFTKADAPPNFRVVPVPSNAFNAPRL 162
Db 144 VGVIGPGSSVAIQVQNLQFNIPQIAYSATSMDLSKTLFKYFMRYVVPVPSDAQOARAV 203
QY 163 ALKEFNWTRVGTYYQNPRLSLPHNMVADLDAME-VEVVTQSFVNDVAE-SLKKLRE 220
Db 204 DIVARYNWTYYSAVH-TEGNTGESGMEAFKDMKAGEICIAHSYKIYSNAGEQSPDKLLK 262
QY 221 KDVRIILGNFNEHFAH-----KAFCEAYKLDYGRAYQLIMATYSTDWNVNTQDSECSVE 276
Db 263 K-----LTSHLPKARVYACFE-----GMTVRGLLA-----MR 291
QY 277 EIATALGAILVDLLPLSTSG-----DIT-----VAGITA-----DEYLVYED 314
Db 292 RLGLAGE-----FLLAGSDWADRYDVTDCYQREAVGGITIKLQSPDVKWFDDYLLKL 345
QY 315 -----RLRG--TEYSRFH-----GYTIDGIW 333
Db 346 PETNHRNPWFQEFQWHRFQRCLEGFPQENSKYKNTCSNLSLTKTHHVDKMGVFINAIY 405
QY 334 AAALAIQYVAEK-----REDLTFHRYVKDWESVFLEALRNTSFEGVTGPVRFY--N 384
Db 406 SMAYGLNHMQMSLCPGYAGLGDAMKPIDGR-----KLLESMLKNTFTGVSGDTILFDEN 459
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QY 385 NERKANILINQFOLGOMEK-----IG-----EYHSOKSHLDLSL-GKP--- 421
Db 460 GDSPGRYEIMNFK--EMGKDYFDYINVSWDNGELKMDDDVWVKRSNIIRSVCPCEK 517
QY 422 --VKWVGK-----TPPKDRTLIYIEHS-----Q 442
Db 518 GQIKVIRKEVSCCWCTCTCKENEYVDFEYTKACQSGSWPTDDLTCGCDLIPVOYLWGD 577
QY 443 VNPTIYIVSASVIGVITATVFLAPNIKYRNORYIKMSSPHLNNLIIVG-----C 493
Db 578 PEPIAAVFAECLGLLTLFTVVVF---IIVRDPVVKSSRELCTIILAGICLGLCTFC 634
QY 494 MIT-----YLSIIFGLDITLSSVAAAPYICTARAWILMAGFSLSFGAMSKTRVHS 546
Db 635 LIAKPKQIYCIYORIGILSP-----AMSALVTKTKTRIAR 671
QY 547 IFTDLKLNKKVKDYOLF--VGVLLAIDAIITWQIADPFPVRETQKLEPLH- 598
Db 672 ILAGSK--KKICTKKPRFMSACAQIVIAFILICIQIIVALEFMEP-----PDIMHD 722
QY 599 HENIDVLVIPENECYQSEHMTIFVSIYAYKGLLVFGAFLAWETRHVSIPA-LNDSKH 657
Db 723 YPSIREVYLI---CNTNLGVVTPL--GYNGLLILSCTFYAFKTRNV--PANFNEAKY 773
QY 658 IGFSYVNVETCLAGRAISLVLSDRKDLVFLLSFFIIFCTTATLCLVFPKLVELKRP 717
Db 774 IAFYTTTCIILWAFVPIYF---GSNYKIITMCFVSLSATVALGCMFVPKVIILAKP 829
QY 718 QGVVDRVRATLR-----PMSKNGRRDSSVCELEOR-----LRD----- 751
Db 830 -----ERNVRSATTSIVVRMHVGDGKSSAASRSSLVNLWKRSGSGETLRNKGKSVTW 885
QY 752 VKNTNC-----RFRKALMEKENELQALI-----RKLP--PARKWIDGVTC 791
Db 886 AQNEKSSRGQHLWQRLSIHNKENPNQAVIKPFPKSTESRGLGPRGAGGSAGVGAT 945
QY 792 GGSNVGSELEPIILNDDIVRLSAPPVREMPSTVTWTSVDSVSTHVMDSNFVSQST 851
Db 946 GGAGCA-----GAGPGGPESPDA----- 963
QY 852 VNAPSLPPKKKQSIVEHSHAPAPMMQ---PIQQOOLQHLQHOQHOQOOLQHOQ 908
Db 964 -----GPKALYDVAEAEHPAPAPRSPSIST----- 992
QY 909 MQOQOQOQHHRHLEKRNVSQAQTDNIGISITAGKRGSGDCSSMRERROSTASRHYD 968
Db 993 -----LSHRAGASRTDDVPSLHSEVPARSSSGSLMEQISSVVTRF-- 1036
QY 969 GSGQTPPARPKYSSSHRNSTNISTSOSELSNMCPSKPTPAVIKPTASDHRRTSMGS 1028
Db 1037 -----TANI-----SELNSMMLSTAAPSPGV-----GA 1059
QY 1029 ALKSNFVV 1036
Db 1060 PLCSYLI 1067

RESULT 9
159362
calcium/polyvalent cation-sensing receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: 159362; A55594
R:Rust, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995
A:Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve
A:Reference number: 159362; MUID:95241465
A:Accession: 159362
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1079 <RES>
A:Cross-references: EMBL:U02089; NID:g790578; PIDN:AACS2195.1; PID:g790579
A:Experimental source: striatal
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QY 52 V--MPSVKLALGHVNEHGKILANRYLRHWNNDTQCNAAVGVKSFDDMMHS----- 99
Db 76 IHRLEAMLYALDQINDPDLNPNVTLGARILDTCSRDTVALEQSLTFVQALIKDTSDDR 135
QY 100 -----GPNKVM-LFGAACHVTDPTAKASKHWHLTQLSYADTHPMFTKDAFPNF 148
Db 136 CTNGEPPVFKPKVGVGVLGSSSSVIMANILRUFQIPQIYSTAPELSDORRYDF 195
QY 149 -RVVPSENAFNAPRLALKFEFNWTRVGVYQNEPRYS----- 184
Db 196 SRVPPDSFQAQAVDIVKALGNVYSTL-ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--MVADLDAVEVEVETQS-----FVNDVAESLKKLREKDVRIILGNFNHFA 235
Db 255 RIPQEKRTIDFRIKOLLPPNSRAVVFAND-----EDIKQIL----- 296
QY 236 RFAFCAYKLDYGRAYOWLMATYSTDMWNTQDSECSVEEATALEGAILVLLPLST 295
Db 297 ----AAAKRADQVGH-FLWV-----GSDSWGSKINPLHQHEDIA---EGAITIQPKRATV 343
QY 296 SG-----DITVAGI-----TADYLVEYDRL-RGPEYS 322
Db 344 EGFDAVFTSRTLENNRNWFAEYWEENFNCKLTISGKKEDTDKCTGQERIGKDSNYE 403
QY 323 RPHG-----YYDGIWAAALAIQYVAEREDLLTHFDYR--VKDMESV-----FLPALRTSF 373
Db 404 Q-EGKVOQVIDAVYAMAHALHHM--NKLCA--DYRGVCPMEQAGGKLLKYIRHVN 457
QY 374 EGVTG-PVRP-YNNERKANLINOFGQMEK-----IGEY--HSQKSHLDLSLGKPKV- 423
Db 458 NGSAGTPVFNKNGDAPGYDIFQYQTTNTNPGYRLIGQWTDDELQNLNEDMOWGKGVRE 517
QY 424 -----WV-----GTPPKDRT----- 434
Db 518 IPSSVCTLPCKQORKKTKGTCCCTCEPCDGYQYQFDEMTQCHQYDORPENRTGQ 577
QY 435 ----LIVIE-HSQVNPTIYIVSASVIGVLIATVF-LAFNIKYRNQRYIKMSSPHLNLI 489
Db 578 NPIPIKLEHNS----PWAVIPVFLAMLG-LIATIFVMAFIRYNDTPIVRASGRELSYVL 632
QY 490 IVGCMITYLSIIFGLDITLSSVAAPF--VICTARAWILMAGSLSGAMFSKTRVHSI 547
Db 633 LTGIFLCYI-ITFL-----MIARPDVAVCFRRVFLGLGMCISYAALLTNTNRIYI 683
QY 548 FTDKLN---KKVIKDYQLFMVGVLLAIDIAITITWQIADP-----FYRETKOLEPLHH 599
Db 684 FEGKSVTAPRLISPTSLATSSLSISVOLLGVFIFWGVDPDPNIIIDYDEHKTMPN- 740
QY 600 ENIDDLVIPENECYQSEHMTIFVSIYAYKGLLVFGAFLEWETRHVSIPALMDSKHIG 659
Db 741 EQARGVL-----KCDITDLQIICSL--GYSILLWVTCTVYAIKTRGV-ENENAKPIG 791
QY 660 FSVYNVFTCLAGAAISLVLSRDLVVF---LLSFIFICTTATLCLVFPVKLVEKRN 716
Db 792 FTMYTTCIIVLAFIPIFFGTAQSAEKLYIQTTLTISMNLSASVALGMLMYPKYIIFH 851
QY 717 PGQVVDKVRRA-----TLRPMK-----NGRDSVCE 744
Db 852 PELNVOKRRSRKAVVTAATMSSRLSHKPSDRPNGEAKTELCE 894
RESULT 7
JC2131
metabotropic glutamate receptor 5 B - human
C:Species: Homo sapiens (nan)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2131
R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131; MUID:94197696.
A:Accession: JC2131

A:Molecule type: mRNA
C;Residues: 1-1212 <MIN>
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F;580-604/Domain: transmembrane #status predicted <TM1>
F;617-637/Domain: transmembrane #status predicted <TM2>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;694-714/Domain: transmembrane #status predicted <TM4>
F;738-759/Domain: transmembrane #status predicted <TM5>
F;773-794/Domain: transmembrane #status predicted <TM6>
F;803-827/Domain: transmembrane #status predicted <TM7>
Query Match 4.3%; Score 278.5; DB 2; Length 1212;
Best Local Similarity 19.7%; pred. No. 1.1e-08;
Matches 224; Conservative 158; Mismatches 368; Indels 389; Gaps 53;
QY 104 VMLFGAACHVTDPTAKASKHWHLTQLSYADTH-PMFTKDAFPNFRVVPVPSNAFNAPRL 162
Db 144 VGVIGPGSSVAIQVNLQLFNFIQAIYSATSMDLSKDTLTKYPMRVVPSDAQOARAV 203
QY 163 ALLKEFNWTRVGVYQNEPRYSPLPHNHVADLDAME-VEVVEQTSFVNDVAE-SLKKLRE 220
Db 204 DIVRYNWTYYSAVH-TEGNTGESGMEAFKDSAKEGICIAHSYKIYSNAGEQSFDKLLK 262
QY 221 KDVRIILGNFNEHFAR----KAFCEAYKLDYGRAYOWLMATYSTDMWNTQDSECSVE 276
Db 263 K-----LFSHLPKARVWACFCE-----GMTVRGLLMA-----MR 291
QY 277 BIATALEGAIVLLPLSTSG-----DIT-----VAGITA-----DEVLYEVD 314
Db 292 RLGLAGE-----FLLGSDGWADRYDYGQREAVGGITIKLQSPDVKWFDFYLLKL 345
QY 315 -----RLRG--TEYSRHH-----GTYVDGIW 333
Db 346 PETHRNPWFQHFQHRFQCRLEGFPQENSKYNTKNSLSLTKTHHVQDSKMGFVINAIY 405
QY 334 AAALAIQYVAEK-----REDLLTHFDYRVKDWESVELEALRNTSFEQVTPGVRFY--N 384
Db 406 SMAYGLHNQMSLCPGYAGLCDAMKPIDGR-----KLLESMLKTNFTGVSGDTILFDEN 459
QY 385 NERKANILINOFQLOQMEK-----IG-----EYHSQKSHLDLSL-GKP--- 421
Db 460 GDSPPRYEIMNFK--EMGKDYFDYINVGSDWNGELKMDDEVWSKKSNIIIRSVCSPECK 517
QY 422 --VKWVGK-----TPPKDRTLIYIEHS-----Q 442
Db 518 GQIKVIRKEGVSCWCTCTPCKENEVYFDEYTCACQOLGSWPTDDLTGCDLIPVQYLRWGD 577
QY 443 VNPTIYIVSASVIGVLIATVFLAFNIKYRNQRYIKMSSPHLNLIIVG-----C 493
Db 578 PEPIAAVVFACLGILLATLFTVTVF---IYRDTVPVKSRSRELCLVILLAGICGLYLTFC 634
QY 494 MIT-----YLSIIFGLDITLSSVAAPFYICTARAWILMAGFSLSGAMFSKTRVHS 546
Db 635 LIAPKQIYCYLQRIQIGLSP-----AMSYALVTKTNRIAR 671
QY 547 IFTDLKLNKKYIKDYQLPM-----VVGVLIAIDIAITITWQIADPPYRETKOLEPLH- 598
Db 672 ILAGSK--KKICTKPRFMSACAQLVIAFIIQGLIIVAFIMEP-----PDIMHD 722
QY 599 HENIDDLVIPENECYQSEHMTIFVSIYAYKGLLVFGAFLEWETRHVSIPA-LNDSKH 657
Db 723 YPSIREVYLI-----CNTNGLGVVTPPL--GYNGLLILSCTFYAFKTRNV--PANENEAKY 773
QY 658 IGFSYVNVFTCLAGAAISLVLSRDLVFLVLSFFIIFCTTATLCLVFPVKLVEKRN 717
Db 774 IAFMYTTCIIVLAFVPIYF---GSNKIITMCFVSLSATVALGCMFVFPKVIILAKP 829
QY 718 QGVVDKVRATILR-----PMKNGRRDSSVCELEORLDRVNTNCRFR-KALM 764
Db 830 ----ERNVRSATTTSTVVRMHVGDGKSSSAASRSSSLVNLWKR-RGSSGETILRYDRRLA 884

Db 48 DITLGLFPVHGRSGKAGCELKKEGTHRLLEAMLFALDRINNDPDLNITLGAIRILD 107
Qy 82 TQCNAAVGVKSFDDMMH-----SG-----PNKVM-LFGAACTHTVDPPIAK 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 108 TCSRDTHALEQSLTFQALIEKDGTEVRGSGGPPIITKPERVVGIVGASGSSVSIWVAN 167
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 121 ASKHHLTQLSVADTHPMFTKDAFPNFF-RVVPSENAFNAPRLALLKEFNWTRVGVYQN 179
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 168 ILRLFKIPQISYASTAPDLSDNSRYDFFRVPSDFYQQAQMDIVRALKNWTVSTL-AS 226
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 180 EPRYSLPHNHMVDLDAVEVEVETQSFND--VAESLKKLRE-----R 220
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 227 EGSYG-----ESGVEAFIOKSRNGGVCIAQSVKIPREPKTGDFDKIIKRLLET 275
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 221 KDVRILGNFNEHFAKFAKCEAYKLDYMYRAYQWLMATYSTDMWNVTQDSECSVEEIAI 280
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 276 SNARGIILIFANEDDIRRVLEAARRANQTGHFF-WM-----GSDSWGSKAPVLRLEVA- 328
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 281 ALEGAILVDLLPLSTSG-----DITVAGITADELYVEYDR---LRGTEYS 322
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 329 --EGAVTILPKRMSVRGDFRYFSRSTLDNRRNINWFAEFWEDNFHCKLSRHALKKGSHIK 386
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 323 RPHG-----YTDGIMAAALAIQVVAEKREKRELLTHEDY-----R 356
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 387 KCTNBERIGQDSAYEQEGKGVQFVIDAVIANGHALHAM-----HRDLCPGRVGLCPR 437
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 357 VKDWESV-FLEALRNTSFGVTG-PVRF-YNNERKANILINQOL-----GOMEKIGEYHS 409
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 438 MDPVDGTQLLKIRNVNFSIAGNPVTFNENGDPGRYDIYQYQLRNGSAEYVIG---S 494
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 410 QKSHLDLSLGKPKVKG-----R 426
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 495 WTDHLHLRIER-MQWPGSQQLPRISICSLPCQPGERKKTVMGACCHCEPCRGYQYQVD 553
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 427 ---KT-----PPKDRTL--IYIEHSQVNPITYIVSASVIGVITATVFLAFN-IKY 472
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 554 RYCTKTCPPYDMRPTENRTSCQPIPIVKLEWSDSPAVLPLFLAVVG-IAATFLVVTVFVRY 612
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 473 RNORIKMSSPHLNLIIVGCMITYLSIIFLGLDITLSSVAAFPYICTARAWILMAGFSL 532
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 613 NDTPIVKAAGRELSYVLLAGIFLCYATTFMLTAEPDLGT-----CSLRIFLGLGMSI 665
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 533 SFGAMFSKTRVHVSIFTDKLN---KKVIKDYQLFMVGVVLLAIDAIITWQIADPF-- 587
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 666 SYAALLTKTNRIRYFEOGKRSVSAPREFISPASQALAITFILSLQLLGCWFWVPDPSHS 725
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 588 ---YRETKOLEPLHE-----NIDDLVLPENECYCOSEHMTIFVSIYAYKGLLVFGAF 639
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 726 VYDFQDQRTLDPRFARGVCLKDISLSLI-----CILGYSMLLMVTCTV 769
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 640 LAWETRHVSIPALNDSKHIGFVSYNVFIITCLAGAAISLVLSDRKDLVFV---LLSFFIIF 696
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 770 YAIKTRGVF-EFNEAKPIGFMTTCIIVLAFIPIFFGTSQSADKLYIOTTLTVSVSL 828
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 697 CTTATLCLVFVKLVKLRNPGQVDRKRA-----TLRPMSE-----NGRDS 741
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 829 SASVSLGMLYMPKVYIILFHPQONVPRKRSKAVVTAATMNSKTQKGNFRNGEAKSE 888
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 742 VCE-LEQRLDVKNT 755
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 889 LCENLETPALATKQT 903
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 4

I49142

metabotropic glutamate receptor 8 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C:Accession: I49142

R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.

J. Neurosci. 15, 3075-3083, 1995

A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory b

A:Reference number: I49142; MUID:95239344

A:Accession: I49142

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-908 <RES>

A:Cross-references: EMBL:U17252; NID:g854728; PIDN:AAA68149.1; PID:g854729

C:Genetics:

A:Gene: mglur8

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: neurotransmitter receptor

Query Match 4.88; Score 305; DB 2; Length 908;
Best Local Similarity 20.7%; Pred. No. 1.8e-10;
Matches 195; Conservative 151; Mismatches 350; Indels 248; Gaps 42;

Qy 4 PSFPPFASLLFLILACGTAKR-----SDVVIAGFRP-YGDGVENSVTG--- 49
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 12 PCFLLTAKFYWIL--TWMOETHSQEYAHSLRDLGDIILGLFPVHAKGERGVPCGDLKK 69
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 50 -RGV--MPSVKALGHVNEHKGILANYRLHMMWNDTCN-----AAVGKSF 93
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 70 EKGHRLLEAMLYAIDQTKDKPDLLSNITLGVRIIDT-CSDTYALEQSLTFVQALIEKDA 128
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 94 FDM-----MHSQPNKVM-LFGAACTHTVDTPIAKSKHHLTQLSYADTHPMFTKDAF 144
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 129 SDVKCANGDPPIFTKPKISGVIGAAASVIMVANILRLFKIPQISYASTAPELSDNTR 188
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 145 PNEF-RVVPSENAFNAPRLALLKEFNWTRVGVYQNEPRYS-----LPHNHMVDLDA 196
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 189 YDFSRVPPDSYQQAQMDIVLWGNVYSTL-ASENGYGESGVEAFTQISREIGVCI 247
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 197 MEVEVETQSFVNDVAESLKKLRE-KDVRIITLGNFNHFARKAFCEAYKLDYMYRAYQWL 255
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 248 AQSQKIPREPFGFEKTIKRLLETPNARAVIMFANEDDIRGILEAAKKNQSGH-FLWI 306
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 256 IMATYSTDMWNVTQDSECSVEEIALEGAALYVLLPLSTSGD-----ITVAGITAD 307
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 307 ----GSDSWGSKAPVYQOEIA---EGA-VTILPKRASIDGFDYFRSRTLANNRN 356
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 308 EYLVEYDLRGTESRPHG-----YTDGIMAAALAI 339
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 357 VWFAEFSQGNFGKSGSGHGRKNSHIKCTGLERIASDSSYEQEGKVQFVIDAVTSMAYAL 416
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 340 -----QVVAEKREDLLTHFDYRVKDWESVLEALRNTSFGVTG-PVRF 382
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 417 HNMHKLCPGYIGLCPRMVITDGKELCY-----IRAVNFGSAGTPVTF 461
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 383 -YNNERKANILINQOLQOME---KIGEYHSQKSHLDLS----- 417
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 462 NENGDAQGRYDIFQYQINNKSTYKIIIGHWTNQLHLKVEDMQWANREHTHPASVCSLPCK 521
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 418 -----LGKPVKW-----VGTTPPKDRT-----LIYIE-HS 441
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 522 PGERKKTVMGVPCVCHGCRCEGYNQVDELSCELCPLDQRPNIINRTGCQRIPIIKLEHWS 581
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 442 QVNPTIVSASASVIGVITATVFLAFNFKYRNQRIKMSPHLNLIIVGCMITYLSII 501
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 582 ----PWAVPVLLIALLGIIATTFVIVRVNDPIVPRASGRELSYVLLTGIFLCY-SIT 636
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 502 FLGLDITLSSVAAFPYICTARAWILMAGFSLSGFAMFSKTRVHVSIFTDKLN---KKVI 558
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 637 FLMI-----AAPDTIICSFRIFLGLCMCFSYAALLTKTNRHRIREFQGGKSVTAPKFI 690
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 559 KDYOLFVWVGVLDAIDAITTQIADP-----PYRETKOLEPLHENDVLPENNEY 613
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 691 SPASQVLTSLISVQLLGVFWFVFPVDPPTIITYGEQRTLDP---ENARGVL-----K 741
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 614 CQSEHMTIFVSIYAYKGLLVFGAFIATWETRHVSIPALNDSKHIGFVSYNVFIITCLAGA 673
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 742 CDISDLSLICSL--GYSILLMWTCVTVAIKTRGVF-EFNEAKPIGFMTTCIIVLAFI 798
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Qy 674 AISLVLSDRKDLVFV---LLSFFIIFCTTATLCLVFPVKLVKLRNPGQVDRKVR----- 726
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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OM protein - protein search, using sw model

Run on: April 30, 2002, 09:59:52 ; Search time 41.85 Seconds
(without alignments)
2220.620 Million cell updates/sec

Title: US-09-715-962-4
Perfect score: 6409
Sequence: 1 MFRPSWPFASLLFLLWST.....SANGQSCPNIKIDIVEYL 1220

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1140.5	17.8	960	2 JE0356	gamma-aminobutyric
2	646.5	10.1	402	2 T29703	hypothetical prote
3	309	4.8	912	2 JH0563	metabotropic gluta
4	305	4.8	908	2 I49142	metabotropic gluta
5	297	4.6	1218	2 S71376	glutamate receptor
6	280.5	4.4	915	2 A49874	metabotropic gluta
7	278.5	4.3	1212	2 JC2131	metabotropic gluta
8	270.5	4.2	1180	2 JC2132	metabotropic gluta
9	265.5	4.1	1079	2 I59362	calcium/polyvalent
10	261.5	4.1	1199	2 A41939	G protein-coupled
11	258.5	4.0	871	2 A46742	metabotropic gluta
12	256	4.0	1171	2 A42916	metabotropic gluta
13	249	3.9	1078	2 A56715	calcium receptor (
14	248.5	3.9	976	2 T51137	ionotropic glutama
15	247	3.9	1088	2 B56715	calcium receptor (
16	246.5	3.8	941	2 T51135	ligand-gated chann
17	246	3.8	872	2 JH0561	metabotropic gluta
18	246	3.8	879	2 JH0562	metabotropic gluta
19	241	3.8	962	2 D86186	hypothetical prote
20	240	3.7	879	2 JC7160	metabotropic gluta
21	237.5	3.7	999	2 T27628	hypothetical prote
22	237	3.7	921	2 T51136	ionotropic glutama
23	237	3.7	923	2 F84732	probable ligand-ga
24	235	3.7	253	2 T29704	hypothetical prote
25	229	3.6	1085	2 S40476	Ca(2+)-sensing rec
26	222	3.5	1267	2 T21340	hypothetical prote
27	218.5	3.4	925	2 T06128	hypothetical prote
28	213.5	3.3	953	2 E84732	probable ligand-ga
29	210.5	3.3	1010	2 T13167	Lola-like protein

ALIGNMENTS

RESULT 1
JE0356
gamma-aminobutyric acid receptor B precursor - human
N;Alternate names: GABA(B) receptor
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 12-Feb-1999
C;Accession: JE0356
R;Grifa, A.; Totaro, A.; Rommens, J.M.; Carella, M.; Roetto, A.; Borgato, L.; Zelante Biochem. Biophys. Res. Commun. 250, 240-245, 1998
A;Title: GABA (gamma-amino-butyric acid) neurotransmission: Identification and fine m
A;Reference number: JE0356; MUID:98440782
A;Accession: JE0356
A;Molecule type: mRNA
A;Residues: 1-960 <GRI>
A;Cross-references: GB:Y11044; NID:g2826760
A;Note: this ORF is not annotated in GenBank entry HSGTHL1, release 109
C;Genetics:
A;Map position: 6p21.3-6p21.3
C;Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;12-960/Product: gamma-aminobutyric acid receptor B #status predicted <MAT>
F;590-613/Domain: transmembrane #status predicted <TM1>
F;627-654/Domain: transmembrane #status predicted <TM2>
F;666-687/Domain: transmembrane #status predicted <TM3>
F;709-730/Domain: transmembrane #status predicted <TM4>
F;767-788/Domain: transmembrane #status predicted <TM5>
F;803-825/Domain: transmembrane #status predicted <TM6>
F;831-856/Domain: transmembrane #status predicted <TM7>
F;23,83,439,481,501,513,630/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 17.8%; Score 1140.5; DB 2; Length 960;
Best Local Similarity 32.4%; Pred. No. 9e-61;
Matches 257; Conservative 167; Mismatches 311; Indels 57; Gaps 16;

Qy 18 WST-----ACGRT--AKRSDVYIAGFFPYGDCVENSYTCRGVMPVSKALCHVNHGKIL 70
Db 149 WSTPKPCQVNRTPHSRRVYIGALFPMGGWPG---GQACQPAVEMALEDVNSRRDIL 205
Qy 71 ANYRLHMWNNDTOCNAAGVGVSFDMHSGPNKVMFGAACHTVDTPIAKASKHWHLTOL 130
Db 206 PDYELKLTHHSKCDPGQATKYLYELLYNDPIKIILM-PCGSSVTLVAEARMNLVL 264
Qy 131 SYADTHP-MFTKADPNFFRVVPSNAPNAPRLALLKEFNWTRVTVYQNEPRYSPLPHNH 189
Db 265 SYGSSSPALSNRQPTFTFTHPSATLHNPTRVKLFEXGWKKIATIQQTTEVFT---- 319
Qy 190 VMAIDLAME-----VEVETQSFVNDVAESLKLKREKDVRIILGNFNEHFAKAFCEA 242
Db 320 --STLLDLEERVKEAGIEITTFRSPFSDPAVPVKNLKRQDARIIVGLFVETEARVFCV 377
Qy 243 YKLDYGRAYQWLIMATYSTDMWNTQDS-ECSVEEIALGAILVDLLPLSTGSDITV 301

ligand gated chann
hypothetical prote
adenomatous polyo
hypothetical prote
atrial natriuretic
natriuretic peptid
A-kinase anchor pr
ionotropic glutama
gene pipsqueak pro
metabotropic gluta
G-box-binding fact
gene pipsqueak pro
hypothetical prote
hypothetical prote
natriuretic peptid
homeotic protein L

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Qy 580 TWQIADPFYRETKQLEPLHHENIDDLVVIPENECYQSEHMTIFVSIYAYKGLLLVFGAF 639
Db 723 TLIIIMEP-----PMPILSYPSIKEYLI-----CNTSNLGVVAPL--GYNGLLIMSCY 769
Qy 640 LAWETRHYSIPA-LNDSKHIGFSVNVETCLAGAAISLVLSDRKDLVFLVLLSFFIIFCT 698
Db 770 YAFKTRNV--PANFNEAKYIAFTMYTTCIIWLAFVPIYF-----GSNYKIITTCFAVSLSV 823
Qy 699 TATLCLVFVPKLVELKRNPGQVVD-----KRVRAATL 729
Db 824 TVALGCMFTPKWYIIIAKPERNVRSFTTSDVVRMHVGDGKLPGRSNTFLNIFERRKAGA 883
Qy 730 RPMSKNGRRDSSVCELEQRLDY-KNTNCRFRKALMEKENEL-----QALIRKLGPEARKW 784
Db 884 GNANENGK---SVSWSEPGGGQVPKGQHMWHLRSVHVKTNETACNQTAIVIKPLTKSYOGS 940
Qy 785 IDGVTCGGS-----NVGSE--LEPILNDDIVRLSAP-----PVRREMPSTTVTMTSVD 832
Db 941 GKSLTFSDTSTKTLYNVEEEDAQPI-----RFSPPGSPSMVVRHRRVPSAATT----- 988
Qy 833 SVTSTHVMENDSFVSQSTVMAPSLPPKKKQSIVEHHSHAPAPTMQPIQQOQQHQQ 892
Db 989 PPLPPLTAETPLFLAEPALPKGLPP-----PLQOQQOQQPPPPQ 1027
Qy 893 HQQMOQ 898
Db 1028 KSLMDQ 1033
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Search completed: April 30, 2002, 10:08:01
Job time: 188 sec

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96029774; PubMed=7476890;
 RA Desai M.A., Burnett J.P., Mayne N.G., Schoepp D.D.;
 RT "Cloning and expression of a human metabotropic glutamate receptor 1
 RT alpha: enhanced coupling on co-transfection with a glutamate
 RT transporter."; Mol. Pharmacol. 48:648-657(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97231349; PubMed=9076744;
 RA Stephan D., Bon C., Holzwarth J.A., Galvan M., Pruss R.M.;
 RT "Human metabotropic glutamate receptor 1: mRNA distribution,
 RT chromosome localization and functional expression of two splice
 RT variants."; Neuropharmacology 35:1649-1660(1996).
 RL CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
 CC ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
 CC THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA (SHOWN HERE) AND BETA;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGUR5.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC
 CC EMBL; U31215; AAA87843.1; -;
 CC EMBL; U31216; AAA87844.1; -;
 CC EMBL; L76627; AAB05337.1; -;
 CC EMBL; L76631; AAB05338.1; -;
 CC GCRdb; GCR_1825; -;
 CC GCRdb; GCR_1826; -;
 CC GCRdb; GCR_1982; -;
 CC GCRdb; GCR_1983; -;
 CC MIM; 604473; -;
 CC InterPro; IPR001828; ANF_receptor.
 CC InterPro; IPR000337; GPCR_Mgr.
 CC Pfam; PF00003; 7tm.3.1.
 CC Pfam; PF01094; ANF_receptor; 1.
 CC PRINTS; PR00248; GPCRMR.
 CC PRINTS; PR00593; MTABOTROPICR.
 CC PRINTS; PR01051; MTABOTROPICR.
 CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
 CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
 CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_5; 1.
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Multigene family; Alternative splicing.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 1194 METABOTROPIC GLUTAMATE RECEPTOR 1.
 FT DOMAIN 19 592 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 593 615 I (POTENTIAL).
 FT DOMAIN 616 629 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 630 650 II (POTENTIAL).
 FT DOMAIN 651 661 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 662 680 III (POTENTIAL).
 FT DOMAIN 681 706 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 707 727 IV (POTENTIAL).
 FT DOMAIN 728 750 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 751 772 V (POTENTIAL).
 FT DOMAIN 773 785 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 786 808 VI (POTENTIAL).
 FT DOMAIN 809 814 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 815 840 VII (POTENTIAL).

FT	DOMAIN	841	1194	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	1014	1035	GLN/PRO-RICH.
FT	DOMAIN	1067	1081	GLN/PRO-RICH.
FT	DOMAIN	1095	1130	ASP/GLU-RICH (ACIDIC).
FT	DOMAIN	1142	1194	SER-RICH.
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	515	515	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	887	906	NSGKSVSWSEPGGGVPGK -> KKQPEFSPSSQCPSAH
FT	VARSPPLIC	907	1194	AOI (IN ISOFORM BETA).
FT	VARSPPLIC	887	906	MISSING (IN ISOFORM BETA).
FT	CONFLICT	593	593	NSGKSVSWSEPGGGVPGK -> KKRQPEFSPSSQCPSAH
FT	CONFLICT	593	593	VOL (IN ISOFORM BETA FROM REF. 2).
FT	CONFLICT	593	593	P -> S (IN REF. 2).
SQ	SEQUENCE	1194 AA; 132376 MW; 970E51AF40584F40 CRC64;		

Query Match 4.3%; Score 276.5; DB 1; Length 1194;
 Best Local Similarity 19.2%; Pred. No. 3e-08;
 Matches 220; Conservative 165; Mismatches 392; Indels 369; Gaps 52;

QY	2	FRPSWFPFASLL-----FLLWSTACGRTRK--SDVYIAGEFF-----PYGDGVENSYT	48
DB	8	FPPAIFLEVSLLPRSPGRKVLLAGASSQSRVARMGDVILGALFVHHQPPAEKVPKRC	67
QY	49	GR-----GV--MPSVKLALGHVNEHGKILANYRLHWMWNTQCNAAVGVKSFDDMH---	98
DB	68	GEIREQYGIQRIEAMFHTLDKINADPVLNPTLGSIRDSCWSSVALQSIETFRDSL	127
QY	99	-----SGPNKM-----LFGAACHVTDPIAKASKHWHHTQLSYAD	134
DB	128	ISTRDEKDGINRCLPDGQSLPPGRTKKPIAGVIGPGSSVVAIQVQNLQLLPQIAYSA	187
QY	135	TH-PMTKDAFNFPRVPSENAFNAPRALALKFENWTRVGTYYQNEPRYSLPHNHVAD	193
DB	188	TSIDLSDKTLKYFLRVPVSDTLQARALMDIVKRYNTVYSAVH-TEGNTYSGMGDAFCE	246
QY	194	LDAME-VEVETQSFVNDVAES-----LKKLRK--DVRILGNFNEHFARKAFCAEY--	243
DB	247	LAQEGLCIAHSDKIYSNAGEKSFDRLLKRLERLPKARVV-----CFEGMTV	296
QY	244	-----KLDMYGRAYOWLMATYSTDMWNVTQDSECSVEEIEATALEGAILVDL----	290
DB	297	RGLLSAMRRLGVVGE-----FSLIGSDGW--ADRDEVIEGYEVEANGGITIKLSPEV	347
QY	291	-----LPLSTSGDITVAGITADEYLVEY-----DRLRGTEYSRF-----	324
DB	348	RSFDDYFLKLRLDTN-----TRNPFPEFQHRFCQRLPGHLLLENPNFKRICTGNES	399
QY	325	-----HGYTDGIIWAAALAIQYV-----AEKREDLLTHFDYRVKDW	361
DB	400	LEENYVODSKMGFVNAIYAMAHGLQNMHIALCPGHVGLCDAMKPID-----G	447
QY	362	SVFLEALRNTSEGTGPVRFYNNERKA-----NILNQFOLGOMEKIGEYHSQKSL	414
DB	448	SKLLDFLIKSSFIGVSGEVEWFEKGDAPGRYDIMNLQVTEANRYDVHVGTWHEGVNI	507
QY	415	D-----LSLGK-----PVK-----WV-----	425
DB	508	DDYKIOMNKGVSRRVSCSEPCLKGOIKVRKGEVSCWICTACKENEYVQDEFTKACDL	567
QY	426	GKTPPKDRT-----LIYIEHQVNPTIYIVSASAVIGVILATVFLAFNFKYRNQRIK	479
DB	568	GWPNADLTGCEPIPVYLEWNIETP-----IIAIFSCGLILVTLFVTLFVLTROTTPVK	624
QY	480	MSSPHNLIIVGCMTIYLSIIFLGLDITLSSVAAPPYIC-----TARAWI--LMA	528
DB	625	SSSRELCTILAG-----IFLG-----YVCPFTLIAKPIPTTSCYLQRLV	664
QY	529	GFS--LSFGAMFSKVRVHSIFTDLKNKKVTKDYOLF-----VGVLLAIDAIT	579
DB	665	GLSSAMCYSLVTKTNRIARILAGSK--KKICTRKPRFMSAWAQVIIASILISVQLTLV	722

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CC EMBL; D28538; BAA05891.1; -
CC EMBL; D28539; BAA05892.1; -
CC EMBL; S64316; AAD13954.1; -
DR GCRDB; GCR_0761; -
DR GCRDB; GCR_1002; -
DR GCRDB; GCR_1003; -
DR GCRDB; GCR_1317; -
DR MIM; 604102; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01055; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1212
FT DOMAIN 22 579
FT TRANSMEM 580 602
FT DOMAIN 603 616
FT TRANSMEM 617 637
FT DOMAIN 638 648
FT TRANSMEM 649 667
FT DOMAIN 668 693
FT TRANSMEM 694 714
FT DOMAIN 715 737
FT TRANSMEM 738 759
FT DOMAIN 760 772
FT TRANSMEM 773 795
FT DOMAIN 796 801
FT TRANSMEM 802 827
FT DOMAIN 828 1212
FT CARBOHYD 88 88
FT CARBOHYD 210 210
FT CARBOHYD 378 378
FT CARBOHYD 382 382
FT CARBOHYD 445 445
FT CARBOHYD 734 734
FT VARSPIC 877 908
SQ SEQUENCE 1212 AA; 132468 MW; A3C7360681C6A25 CRC64;

Query Match 4.3%; Score 278.5; DB 1; Length 1212;
Best Local Similarity 19.7%; Pred. No. 2.3e-08;
Matches 224; Conservative 157; Mismatches 369; Indels 389; Gaps 53;

QY 104 VMLFGAACHVTVDPIAKASHWHLTOLSYADTH-PMFTKDAFPNFRVPSENAFAPRL 162
DB 144 VGVIGPSSVAIQVONLQLFNIPQIAYSATSMDSKTLFKYFMRVFSDAQARAV 203

QY 163 ALLKEFNWTRVGVYQNEPRYSLPHNHVADLDAME-VEVVTQSFDVDAE-SLKRLRE 220
DB 204 DIVKRYNWTIVYSAVH-TEGNYGESGMEAFKDKSAKEGICIAHSYKIYSNAGEQSFDKLK 262

QY 221 KDVRIILGNFNEHAR-----KAFCEAYKDMYGRAYQWLIIMATYSTDWNVNTQDSSECV 276
DB 263 K-----LTSHPKARVVACFCE-----GMTVRGLLMA-----MR 291

QY 277 ETATALEGAILVDLLPLSTSG-----DIT-----VAGITA-----DEYLYEYD 314
DB 292 RLGLAGE-----FLLIGSDGWDADYDVTGQYREAVGGITIKLQSPDKWFDYILKLR 345

QY 315 -----RLRG--TEYSRHF-----GYTDGIW 333
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DB 346 PETNHRNPFQEFQWHRFQCRLEGFPQENSKYNKTCNSSLTALKTHHVQDSKMGFVINALY 405
QY 334 AAALAIQVAAEK-----REDLLTHFDYRVKDWESVLEALRNTSFEGVTPGVREY--N 384
DB 406 SMAYGLHNQMSLCPGYAGLCDAMPIDGR-----KLLLESLMKNFTVSGDITLFDEN 459
QY 385 NERKANILINOLFQGMKEK-----IG-----EYHSOKSHLDLSL-GKP--- 421
DB 460 GDSPGRYEIMNFK--EMGKDYFDYINVGSWONGELKMDDDEYVWSKKSNIIRSVCSPECK 517
QY 422 --VKWVGK-----TPPKDRTLIYIHS-----Q 442
DB 518 GQIKVIRKEVSCCWTCTPCKENYEVDFEYTCACQLGSWPTDGLTCDLIPVQYLWGD 577
QY 443 VNPTIIVSASASVIGVIIATVFLAFNKNRYNORVYIKMSSPHLNLIIVG-----C 493
DB 578 PEPIAAVVFACGLGLATLFTVTVVF--IYRDTPVVKSRELXYIILAGICLGYLCTFC 634
QY 494 MIT-----YLSIIFLGLDITLSSVAAPPYICTARAWILMAGFSLSGFAMFSKTRVHVS 546
DB 635 LIAKPKQIYCYLQRIIGLSP-----AMSYALVTKTNRAR 671
QY 547 IFTDLKLNKKVIKDYQLFM-----VGVLLAIDIAIITTWQIADPFYRETQKLEPLH- 598
DB 672 ILAGSK--KKICTKPRFMSACAQLVIAFILICIQLGIIVAFIMEP-----PDIMHD 722
QY 599 HENIDDLVIPENYEQSEHMTIFVSIYAYKGLLIVFCGLAFWETRHYSIDA-LNDSKH 657
DB 723 YPSIREVYLI-----CNTNLGVVTPPL--GYNGLLILSTCTFYAFKTRNV--PANFNEAY 773
QY 658 IGFSVYNVFTICLAGAAISLVLSDRKDLVFLVLSFFIIFCTTATLCLVFPKLVLEKRN 717
DB 774 IAFWTYTTIILWAFVPIYF-----GSNYKIITMCFSVLSATVALGCMFVPIILAKP 829
QY 718 QGVVDKRVATLR-----PMSKNGRRDSVCELEORLRLRVKNTNCRFR-KALM 764
DB 830 ---ERNVRSAPFTTSTVVRMHVGDGKSSSAASRSSLVNLWKR-RGSGSETLRYKDRRLA 884
QY 765 EKENELQALIRK--LGPEARKWIDGVTCTGSGNVGSELEPILNDDI-----VRLSAPP 815
DB 885 QHKSIECTFPKGSWG-----NGRATMSSNGSKSVTWAQNEKSSRGHLMWRLSIHI 937
QY 816 VRREPMSTVTMTSVDVSPTS-----THVEMDNFSVSVQSTVMA-----PSLPP--K 860
DB 938 NKKNPNQTAIVIKPFKSTESRGLGAGAGAGSAGCGVATGAGCAGACGPGGEPDAGP 997
QY 861 KKKQSIVEHHSHAPAPTMMQ-----PIQQQLQHLQHQHQHQHQHQHQHQHQHQHQHQ 917
DB 998 KALYDVAEAEHFPAPRPSPIST-----1024

QY 918 HHRHLEKRNVSQAOTDDNIGSITSTAGKXRGDCSSMRERROSTASRHYDSQSQTPTAR 977
DB 1025 -----LSHRAGASRTDQDDVPSLHSEPVARSSSQSGSLMEQISVVVTRF----- 1068
QY 978 PKYSSSHRNSNSTISQSELSNMCPSHPSTPAVTKTPTASDHRRTSMGSAKLSNFV 1036
DB 1069 -----TANI-----SELNMLSTAPSPGV-----GAPLCSSYLI 1099

RESULT 15
MGR1_HUMAN
ID MGR1_HUMAN STANDARD; PRT; 1194 AA.
AC Q13255; Q13255; Q14757; Q14758;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 1 PRECURSOR.
GN GRM1 OR GRPCL1 OR MGLUR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
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DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00982; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
Multigene family; Olfaction.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 591 615 I (POTENTIAL).
FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 628 648 II (POTENTIAL).
FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 675 III (POTENTIAL).
FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 703 723 IV (POTENTIAL).
FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 754 775 V (POTENTIAL).
FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 810 VI (POTENTIAL).
FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 826 850 VII (POTENTIAL).
FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 915 AA; 102231 MW; F28AFC46454A6C2 CRC64;
Query Match 4.4%; Score 280.5; DB 1; Length 915;
Best Local Similarity 20.7%; Pred. No. 1.2e-08;
Matches 195; Conservative 145; Mismatches 334; Indels 269; Gaps 48;
QY 7 PPSASLFLFLWSTACGRGTA-----RSDVYIAGFFP-YGDGVNSVYTG-----RG 51
Db 16 FPCCVLEVLVCLVAAAAGQEMAPHSIRIGDVTGLGLFPVHAKGPGSGVPCGDIKRENG 75
QY 52 V--MPSVKLALGHVNEHGKILANYRLHWMNDTCNAAGVGVKSPFDMHMS----- 99
Db 76 IHRLEAMLYALDQVNSDNLNPNVTLGARILDTCSRDTYALEQSLTFVQALIQKDTSDVR 135
QY 100 -----GNPKVM-LFGAACHTVTDPIAKASKWHLTLQLSYADTHPMFTKDAFPNFF 148
Db 136 CTNGEPPVFKPKVGVGAGSSVSMVANILRLFOIPQISYASTAPELSDRRYDF 195
QY 149 -RVVPSNAPNAPRLALKENWTRVGVYQNEPRYS----- 184
Db 196 SRVVPDSFOQAQMDIVKALGNVYSTL-ASEGSYGEKGVESFTQISKEAGGLCIAQSV 254
QY 185 -LPHNH--WVADLDAMEVEVYETOS-----FVNDVAESLKKLREKDVRIILGNHEHA 235
Db 255 RIPOERKDRITDFRIILKQLDTPNSRAVIFAND-----EDIKQL----- 296
QY 236 RKAFCEAYKLDVGRAYQWLIMATYSTDMVNTODSECSVEEATALBGAAILVLLPLST 295
Db 297 -----AAKRAQOVGH-FLWV-----GSDSWGSKINPLHQHEDIA--EGATIQPKRATV 343
QY 296 SG-----DITVAGI---TADYLVYEDRL-RGTEYS 322
Db 344 EGFDAVFTSRLENNRRNWFAYEENFNCKLTISGSKEDTDKCTGQERIGKDSNVE 403
QY 323 RFHG---YTDGIWAALATQYAEKREDLLTHFDYR--VKDWESV---FLEALNFTSF 373
Db 404 Q-EGKQVQFVDVAYAMAHLLHM---NKDLCA--DYRGVCPMEQAGGKKLLKYIRHNF 457
QY 374 EGYTG-PVRF-YNNERKANILINQFQGMKEK-----IGEV--HSQKSHLDLSLGGPKVK- 423
Db 458 NGSAGTPVMENKNGDAPCRDYDFQITNTNPGYRLIGQWTDQLNIEDMQWQKGVRE 517
QY 424 -----WV-----GKTPPKDRT--- 434
Db 518 IPSSVCTLPCKPGKRYTKGTGTPCWTCEPCDGYQYQFDEMTCQHCYPDQRPNERTCGQ 577

QY 435 ---LIVIE-HSQVNPTIIVSASASVIGVITATVF-LAFNIKRYNRQYIKMSSPLNLI 489
Db 578 NIPILKEWHS---PWAVIPVFLAMLG-IATIFVATFIRYNDTPIVRASGRELSQL 632
QY 490 IVCMTIYLSIIFLGLDFTLSSVAAPF--YICTARAWILMAGFSLSGAMFSGKTRVHSI 547
Db 633 LTGIFLCYI-ITEL-----MIAKPDVAVCSFRRVFLGLGMCISYAALITKTNRIVR 683
QY 548 FTDKLN---KKVYKDYQLEWVGVLLAIDIAIITTHQIADP-----FYRETKOLEPLH 599
Db 684 FEQKKSVTAPRLISPTSQLAITSSLSVQLLVGFVWFGVDPNIIIDYDEHKTMP--- 740
QY 600 ENIDDDVLIPENECYQSEHMTIFVSIYAYKGLLLVFGAFLEWTRHVSIPALNDSKHIG 659
Db 741 EQARGVL-----KCDITDLOIICSL--GYSILLMVTCTVYVATKRGVP-ENFNEAPIG 791
QY 660 FSVYNNVITCLAGAAISLVLSDRKDLVF---LLSFFIIFCTTATCLVFPVKLVELKRN 716
Db 792 FTWYTCIVWLAFIPFPGTAQSAEKLYIQTTLTISMNLSASVALGMLYMPKVYIIFH 851
QY 717 PQGVVDKRVRA-----TLRPMK-----NGRRDSSVCE 744
Db 852 PELNVQKRKRKFVAVVTAATMSSRLSHKPSDRPNGEAKTELCE 894
RESULT 14
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ID MGR5_HUMAN STANDARD; PRT; 1212 AA.
AC P41594;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 PRECURSOR.
GN GRM5 OR GPRC1E OR MGLUR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP Katsuki F.;
RC TISSUE=Brain;
RX MEDLINE=94197696; PubMed=7908515;
RA Minakami R., Katsuki F., Yamamoto T., Nakamura K., Sugiyama H.;
RT "Molecular cloning and the functional expression of two isoforms of
human metabotropic glutamate receptor subtype 5";
RL Biochem. Biophys. Res. Commun. 199:1136-1143(1994).
RN [2]
RP REVISIONS.
RA Katsuki F.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 860-952 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93343913; PubMed=7688218;
RA Minakami R., Katsuki F., Sugiyama H.;
RT "A variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon";
RL Biochem. Biophys. Res. Commun. 194:622-627(1993).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
CHLORIDE CURRENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
32 RESIDUES.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way

FT TRANSMEM 703 723 IV (POTENTIAL).
 FT DOMAIN 724 753 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 754 775 V (POTENTIAL).
 FT DOMAIN 776 788 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 789 810 VI (POTENTIAL).
 FT DOMAIN 811 825 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 826 850 VII (POTENTIAL).
 FT DOMAIN 851 915 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 486 486 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 572 572 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 433 433 Y -> F.
 FT /FTIG=VAR_003584.
 SQ SEQUENCE 915 AA; 102250 MW; CFF94E06BF7F4919 CRC64;

Query Match 4.5%; Score 286.5; DB 1; Length 915;
 Best Local Similarity 20.8%; Pred. No. 5.6e-09;
 Matches 196; Conservative 144; Mismatches 334; Indels 269; Gaps 48;

Qy 7 PFASLLFLLWSTACGRGTAK-----RSDVYIAGFFP-YGDGVENSYTG-----RG 51
 Db 16 PFCCVLEVLALAAARQEMVAPHISRIEGDVLGLGFPVIAKGPSGVPCGDIRENG 75
 Qy 52 V--MPSVKLALGHVNEHGKILANYRLHMMWMDTQCNAAVGVKSFDDMHSS----- 99
 Db 76 IHRLEAMLYALDQINSDPNLLPNVTLGARILDTCSRDYVALEQSLTFVQALIQKDTSDVR 135
 Qy 100 -----GNKVM-LFGACTHTVDPIAKASKIWHLTOLSYADTHPMFTKADPNFF 148
 Db 136 CTNGEPFVFKPKVGVVIGASGSSVSIMVILRFQIQAISYASTAPSLSDRRYDF 195
 Qy 149 -RVVSENAFNAPRLALKKEFNWTRGVTVQNEPRYS----- 184
 Db 196 SRVPPDSFQAQAWDVIKALGNVYSTL-ASEGSTGKGVESFTQISKAPGGLCIAQSV 254
 Qy 185 -LPHNH--MVADLDAMEVEVETQS-----FVNDVAESLKLKREKDVRIILGNFNEHFA 235
 Db 255 RIPOERKORTIDFDRIIKQLDTPNSRAVVFAND-----EDIKQIL----- 296
 Qy 236 KKAFCAYKLDYGRAYQWLIMATYSTDMWNTQDSECVSEETATALEGAILVDLLPLST 295
 Db 297 ----AAKRADQVGH-FLWV-----GDSWGSKINPLHQHEDIA-----EGAITIQPKRATV 343
 Qy 296 SG-----DITVAGI---TADVIVEVDRL-RGEYS 322
 Db 344 EGFDAFTSRTLENNRNWVFABYWEENFNCKLTISGSKEDTDRCKTQGERIGKDSNYE 403
 Qy 323 RFHG---YTDGIWAALAIQYVAEKREDBLLTHFYR--VKDWESV-----FLEALRNTSF 373
 Db 404 Q-EGKVQFVIDAVYAMAHALHM--NKLCA--DYRGVCPMEQAGGKLLKYIRNVNF 457
 Qy 374 EGVTG-PVRF-YNNERKANILNQFOLGOMEK-----IGEY--HSOKSHLDLSLGRPKV- 423
 Db 458 NGSAGTPVMFNKNGDAPGRYDIFQYQTTNTSPGRLIGOWTDQLQINIEDMOWGKVRE 517
 Qy 424 -----WV-----GKTPPKDPT--- 434
 Db 518 IPASVCTLPCKGQRKKTQKTPCCPCBPCDGYQFQEDMTQCHQPDYDORPNERNGCQ 577
 Qy 435 ---LIYIE-HSQVNPITYIVSASASVIGVITATVF-LAFNIKYRNORYIKMSPHLNLI 489
 Db 578 DIPIIKLEWHS---PWAVIPVFLAMLG-LIATIFVWATFIRYNDPIVRASGRLSYVL 632
 Qy 490 IVGCMTYLSIIFLDLDTLSSVAAPP--YICFARAWILMAGFSLSGFAMFSKTRVHSH 547
 Db 633 LTGIELCYI-ITFL-----MIAPDPVAVCSFRFVFLGLGMCISVAALLTKTNRIYRI 683
 Qy 548 FTDLKLN---KKVIRKDYQLFMVGVVGLLADIALITITWQIADP-----FYRETKOLEPLHH 599
 Db 684 FEQGKSVTAPRLISPTSQLAITSSLSVOLLGVFWFGVDPDPNIIIDYDEHKTMNP--- 740

Qy 600 ENIDDLVLPENECQSEHMTIFVSIYAYKGLLLVFGAFLAWETHRVHSIPALNDSKHIG 659
 Db 741 EQARGV-----KCDITDLQILICSL--GYSILLMTCTVVAIKTRGVP-ENFNEAKPTG 791
 Qy 660 FSVYNVETICLAGAISLVSDRDLVFEV---LLSFFIIFCTTATLCLVFEVPLKVELKEN 716
 Db 792 FTYMTTCIVWLAFIPFFGTQSAEKLYIQTTLTISMNLSASVALGMDLMPKVIYIIIPH 851
 Qy 717 PQGVVDKRVRA-----TLRPMK-----NGRRDSSVCE 744
 Db 852 PELNVQKRKRSEKAVVTAATMSSRLSHKPSDRPNGEAKTELCE 894

RESULT 13
 MGR7_RAT
 ID MGR7_RAT STANDARD; PRT; 915 AA.
 AC P35400;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
 GN GRM7 OR GPRCIG OR MGLUR7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
 RX MEDLINE=94117433; PubMed=8288585;
 RA Okamoto N., Hori S., Akazawa C., Hayashi Y., Shigemoto R.,
 RA Mizuno N., Nakanishi S.;
 RT "Molecular characterization of a new metabotropic glutamate receptor
 mGluR7 coupled to inhibitory cyclic AMP signal transduction.";
 RL J. Biol. Chem. 269:1231-1236(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Olfactory bulb;
 RX MEDLINE=94195260; PubMed=8145723;
 RA Saugstad J.A., Kinzie J.M., Mulvihill E.R., Segerson T.P.,
 RA Westbrook G.B.;
 RT "Cloning and expression of a new member of the L-2-amino-4-
 phosphonobutyric acid-sensitive class of metabotropic glutamate
 receptors.";
 RL Mol. Pharmacol. 45:367-372(1994).
 CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
 IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
 ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED THROUGHOUT THE BRAIN.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC STRONGEST, TO MGLUR4.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D16817; BAA04092.1; -;
 DR EMBL; U06832; AAA20655.1; -;
 DR GCRDb; GCR_0945; -;
 DR GCRDb; GCR_0946; -;
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF00003; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PRINTS; PR00248; GPCRMR.
 DR PRINTS; PR00593; MTABOTROPICR.
 DR PRINTS; PR01057; MTABOTROPIC7R.
 DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

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FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 491 491 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 524 524 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 976 AA; 108457 MW; 2C17B1F9005AF68 CRC64;

Query Match 4.5%; Score 289.5; DB 1; Length 976;
Best Local Similarity 19.3%; Pred. No. 4.1e-09;
Matches 172; Conservative 130; Mismatches 344; Indels 245; Gaps 31;

QY 30 DVIYAGFPYGDGVNSVTG-----RGV--MPSVKALGLHGVNEHGKILANYLRHLMWMDT 82
Db 44 DIILGLFPVHEKGEKGPVNRGVRLEAMLYAIDRVNNDPNILPGITIGVHILDT 103
QY 83 QCNAAGVKSFDDMMHSGPNKVMLEAGACTHTDP----- 117
Db 104 CSRDTYALNQSLQVFRASLNLDTSYECADGSSPQLRKNASSGPFVGVIGGSYSVSLQ 163
QY 118 IAKASKHWHLTQLSYADT--HPMFTKDAFPNFRVVPSENAFAPRLALLKEFNWTRVGTV 176
Db 164 VANLLRLHFIPQVSPASTAKTSLDKTRFDLFARVPPDTFQSVVALVDILKFNWSTVSTI 223
QY 177 YQ--NEPRYSLPHNHMADLDAMEVEVVE-----TQSFVNDVAESLKK-----L 218
Db 224 HSEGSYGEYGEALHKEATERNVCIKVAEKVPSAADRVFDSIISKLOKKNARGVWLFT 283
QY 219 REKDVRIILGNFNEHFARKACEAYKLDYGRAYOWLMYASTDWNVTQSEGSVEBI 278
Db 284 RAEDARRIL-----QAAKRANLSQPFHWI-----ASDGWKGQKQLLEGLEDI 325
QY 279 ATALEGALLVD-----LPLSTSGDIT 300
Db 326 A---EGALTVELOSEIADFRYMMQMLTPENRNPWFPAETWEDFNCLVTLSTLKVDPDS 382
QY 301 VAGITADEYL-----VEYD---RLR---GTEYSRFHGYTYDGIWAAALAI----- 339
Db 383 NSANSTDNKIGKAKTECDSDSYRLSEKVGVEQESKTQFVVDVAVAFAYALHNLHNDRCNT 442
QY 340 --QVVAEKREDLLHP-----DVRKDWESVFLBALNNTSEGVGTG--PV 380
Db 443 QSDQTTTRKHLOSESVMYRKISTDKSQACPDMANYGKFEFNNYLLNVSFIDLAGSEV 502
QY 381 RF-----YNNERKANI-----LINQFOLQGMEXIGEYHSHKSLDLSL 418
Db 503 KFDROGDGLARYDILNLTQVQENSSGYQYKVGKFWNGLOLNSFVWNKETEQPTSAACS 562
QY 419 -----GKPVKW-----GKTPPKDRTLIY---IEHSQV 443
Db 563 PCEVGMKKQGDTCWCIDSCSEFVYVDEFTCKDCGGLWPYADKLSYALDIQYMKW 622
QY 444 NPTIYVSASASVIGVIAITVFLAFNINQRYKRNQYIKMSSPHLNLIIVGCMITYLSIPL 503
Db 623 NSLFALIPMAIAFGIALTSIVILFAKNHDTPLVRASGRELSYTLFLGILVCYCNTAL 682
QY 504 GLDPTLSSVAAPFYICARAWILMAGESLSFGAMFSKTRVHSIFTDLKLK---KVIKD 560
Db 683 IAKPTIGS-----CVLQREGIGVGSFIYSALLTKNRISFRIFSHASKSAQRUKYISP 735
QY 561 YQLFMVGVLLAIDAIITTTQIADP-----FYRETQKLEPLHENDIDVLPENYEQCS 616
Db 736 OSQVWITSIAIOVLTMVWVPEPCTRYYPDR-----EVIL-----KCKI 780
QY 617 EHMTIFVSIYAYKGLLVFGAFLAWETRHVSIPA--LNSDKHIGFSVYNVFITCLAGAAI 675
Db 781 QDMSFLESQ--YNNILITICTIYAIKTR--KIPENFENESKFIGTMYTTCIIWLAFAPI 836
QY 676 SLVLSDRKDLVFLLSFIIFCTTATICLVFVPKLVKLRNPQGVVDKRV 726
Db 837 YFGTGNSEYQTTTLCISISLASVALVCLYSPKVIYLVFHP-----DKNVR 883

RESULT 12
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MGR7_HUMAN
ID MGR7_HUMAN STANDARD; PRT; 915 AA.
AC Q14831.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR.
GN GRM7 OR GPRC1G OR MGLUR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96437220; PubMed=8840028;
RA Makoff A., Pilling C., Harrington K., Emson P.;
RT "Human metabotropic glutamate receptor type 7: molecular cloning and
RT mRNA distribution in the CNS.";
RL Brain Res. Mol. Brain Res. 40:165-170(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rokey P.K., Burgett S.G., Arnold J.S.,
RA Rostek P.R. Jr., Johnson B.G., Schoep D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY AREAS OF THE BRAIN,
CC ESPECIALLY IN THE CEREBRAL CORTEX, HIPPOCAMPUS, AND CEREBELLUM.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR4.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X94552; AAC64245.1; -
DR EMBL; U92458; AAB51763.1; -
DR GCRDb; GCR_1890; -
DR GCRDb; GCR_2071; -
DR MIM; 604101; -
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01057; MTABOTROPICR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS02599; G_PROTEIN_RECEP_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family; Olfaction; Polymorphism.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 915 METABOTROPIC GLUTAMATE RECEPTOR 7.
FT DOMAIN 33 590 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 591 615 I (POTENTIAL).
FT DOMAIN 616 627 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 628 648 II (POTENTIAL).
FT DOMAIN 649 654 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 655 675 III (POTENTIAL).
FT DOMAIN 676 702 CYTOPLASMIC (POTENTIAL).
```



```
QY 145 PNEF-RVVPSENAFNPRLALLKEFNTRVGTVYQNEPRYS-----LPHNHMVADLDA 196
Db 189 YDFSRVVPDSYQAQAWDIVTALGNVYSTL-ASEGNYGESGVEAFTQISREIGGVCY 247
QY 197 MEYEVVETQSFVNDVASELKLRE-KDVRIITLGNFNHFARKAFCEAYKLDWYGRAYOWL 255
Db 248 AQSQKTPREPRPEFEKIIKRLLETPNARAVIMFANEDDINGILEAAKLNQSGH-FLWI 306
QY 256 IMATYSTDMNVNTQDSCSEVEEIALEGAILVLLPLSTSGD-----ITVAGITAD 307
Db 307 -----GSDSGKSIAPVYQEEIA---EGA--VTILPKRASIDGDFRYSRSTLANNRN 356
QY 308 EYLVEVDRLRGTEYSRPHG-----YTYGIGWAAALAI 339
Db 357 VWFAPFSEGNFGKSGSHGRNSHIKKTGLERTARDSYBQEGKQVQVDAVYSMAVAL 416
QY 340 -----OYAEKREDLTHFDYRVKDWESVLEALRNTSEFSGVTG-PVRF 382
Db 417 HNMHKELCPGYIGLCPRWITIDGKELGY-----IRAVNFGSAGTPVTF 461
QY 383 -YNNERKANILINOFQLGOME---KIGEYHSQKSHLDLS----- 417
Db 462 NENGAPGRVDIFQYQINNKSSTEYKIIIGHWTNQLHKVEDQWANREHTHPASVCSLPCK 521
QY 418 -----LCKPVK-----VGKTPPKDRT-----LVIIE-HS 441
Db 522 PGERKKTGVGPCWHGCRGEGYNYQVDELSCELCPDQRPNIINRTGCRPIPIKLEWHS 581
QY 442 QVNPTIIVSASVIGVITATVFLAFNIKRYNORYIKMSSPHLNLLIIVGCMITLSII 501
Db 582 ----PHAVPVLIALIGIATTFVIVFVRYNDPIVRASGRELVSYLTLTGIFLCY-SIT 636
QY 502 FLGLDTLSSVAAPFYICTARAWILMAGFSLSFGAMFSKTRVHRSIETDLKLN---KKVI 558
Db 637 FLMI-----AAPDTICSFRRIFLGLGCMCFSYAALLTKTRIHRIFPQKKSVTAPRFI 690
QY 559 KDQLFVWGVVGLAIDAITTWOIADP-----FYRETKQLEPLHHEHNDIVLVIPENEY 613
Db 691 SPASQLVITFSLISVQLLVGFVFMVVDPPHTIIDYGEQRTLDP---ENARGVL-----K 741
QY 614 QQSEHMTIFYSIIYAYKGLLLVFGAFLAWETRHVSIPALNDSKHIGFSVYNVETITLAGA 673
Db 742 CDSIDSLISLCL--GVSILLMVTCTVVAIKTRGVP-ETFEAKKPIGFTMYTTCIWLAFI 798
QY 674 AISLVLSDRKDLVFV---LLSFFIIFCTTATCLVFPVKLVELKRNPGQVYDKRVR---- 726
Db 799 PIFFGTAQSAEKMYIQTTLTVSMLSLSASVSLGMLYMPKVYIIIFHPQNVQKRKRSPKA 858
QY 727 ----ATL-----RPMKNGRRDSSVCE-LEQRLRDVKNT 755
Db 859 VVTAATMQSKLIQGNDRP-----NGEVKSELCSLETNTSSTKTT 899

RESULT 10
MGR4_HUMAN
ID MGR4_HUMAN STANDARD; PRT; 912 AA.
AC Q14833;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 4 PRECURSOR.
GN GRM4 OR GPRC1D OR MGLUR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
RX MEDLINE=96346635; PubMed=8738157;
RA Makoff A., Leichuk R., Oker M., Harrington K., Emson P.;
RT "Molecular characterization and localization of human metabotropic
```

```
FT glutamate receptor type 4."
RL Brain Res. Mol. Brain Res. 37:239-248(1996).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=98141892; PubMed=9473604;
RA Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S.,
RA Rosteck P.R. Jr., Johnson B.G., Schoepf D.D., Belagaje R.M.;
RT "Group III human metabotropic glutamate receptors 4, 7 and 8:
RT molecular cloning, functional expression, and comparison of
RT pharmacological properties in RGT cells.";
RL Brain Res. Mol. Brain Res. 53:88-97(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95342351; PubMed=7617140;
RA Flor P.J., Lukic S., Rueegg D., Leonhardt T., Kneffel T., Kuhn R.;
RT "Molecular cloning, functional expression and pharmacological
RT characterization of the human metabotropic glutamate receptor type
RT 4.";
RL Neuropharmacology 34:149-155(1995).
CC -!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN THE CEREBELLUM.
CC EXPRESSED AT LOW LEVELS IN HIPPOCAMPUS, HYPOTHALAMUS AND
CC THALAMUS. NO EXPRESSION DETECTED IN LIVER.
CC -!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC STRONGEST, TO MGLUR6.
CC -----
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CC -----
DR EMBL; X80818; CAA56784.1; -
DR EMBL; U92457; AAB51762.1; -
DR GCRDb; GCR.1891; -
DR GCRDb; GCR.2069; -
DR MIM; 604100;
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; PR00248; GPCRMR.
DR PRINTS; PR00593; MTABOTROPICR.
DR PRINTS; PR01054; MTABOTROPIC4R.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Multigene family.
FT SIGNAL 1 32
FT CHAIN 33 912
FT DOMAIN 33 587
FT DOMAIN 588 610
FT DOMAIN 611 624
FT TRANSMEM 625 645
FT DOMAIN 646 656
FT TRANSMEM 657 675
FT DOMAIN 676 699
FT TRANSMEM 700 720
FT DOMAIN 721 750
FT TRANSMEM 751 772
FT DOMAIN 773 785
FT TRANSMEM 786 808
FT DOMAIN 809 821
FT TRANSMEM 822 847
FT DOMAIN 848 912
FT CYTOPLASMIC (POTENTIAL).
FT METABOTROPIC GLUTAMATE RECEPTOR 4.
FT EXTRACELLULAR (POTENTIAL).
FT I (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT II (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT III (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT IV (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT V (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
FT VI (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT VII (POTENTIAL).
FT CYTOPLASMIC (POTENTIAL).
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QY 735 NGRDSSVCELEORLRVDKNTNCRFRKALMEKENELQALIRKL 777
Db 910 TNNNE-----EKSRLLEKENRELEKIAEKEERVSELHQH 946

RESULT 6

MGR8_RAT
ID MGR8_RAT STANDARD; PRT; 908 AA.
AC P70579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR.
GN GRM8 OR GPRC1H OR MGLUR8.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97168760; PubMed=9016353;
RA Saugstad J.A., Kinzie J.M., Shinohara M.M., Segerson T.P.,
RA Westbrook G.L.;
RT "Cloning and expression of rat metabotropic glutamate receptor 8
RT reveals a distinct pharmacological profile."
RL Mol. Pharmacol. 51:119-125(1997).
CC -I- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
CC IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
CC ACTIVITY.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: PROMINENT EXPRESSION IN OLFACTORY BULB,
CC PONTINE GRAY, LATERAL RETICULAR NUCLEUS OF THE THALAMUS, AND
CC PIRIFORM CORTEX. LESS ABUNDANT EXPRESSION IN CEREBRAL CORTEX,
CC HIPPOCAMPUS, CEREBELLUM, AND MAMMARY BODY.
CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U63288; AAB09537.1; -
CC GCRDB; GCR_1411;
CC InterPro: IPR001828; ANF_receptor.
CC InterPro: IPR000337; GPCR_Mgt.
CC Pfam; PF00003; 7tm_3; 1.
CC Pfam; PF01094; ANF_receptor; 1.
CC PRINTS; PR00248; GPCRMR.
CC PRINTS; PR00593; MTABOTROPICR.
CC PRINTS; PR01058; MTABOTROPICR.
CC PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC Multigene family; Olfaction.
CC
CC SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 908 METABOTROPIC GLUTAMATE RECEPTOR 8.
FT DOMAIN 34 583 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 584 608 I (POTENTIAL).
FT DOMAIN 609 620 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 621 641 II (POTENTIAL).
FT DOMAIN 642 647 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 648 668 III (POTENTIAL).
FT DOMAIN 669 695 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 696 716 IV (POTENTIAL).
FT DOMAIN 717 746 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 747 768 V (POTENTIAL).
FT DOMAIN 769 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 803 VI (POTENTIAL).

FT DOMAIN 804 818 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 819 843 VII (POTENTIAL).
FT DOMAIN 844 908 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 452 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 565 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 908 AA; 101866 MW; FCAB54CB8E3DD915 CRC64;

Query Match

Best Local Similarity 4.9%; Score 316; DB 1; Length 908;

Matches 196; Conservative 159; Mismatches 340; Indels 250; Gaps 45;

QY 4 PSWFFPASLFLLLWSTACGRTRAKR-----SDVYIAGFFP-YGDGVENSYTG--- 49
Db 12 PCFFLLTAKFYWL--TMMQTHSQEYAHVIRVDGDIILGLFPVHAKGERGVPCGLKK 69
QY 50 -RGV---MPSVKLALGHVNEHGKILANYRLHMMNDTCN-----AAGVKSF 93
Db 70 EKGIRLEAMLYAIDQINKDPDLLSNITLGVRLDT--CSRDTYALBQSLTFVQALIEKDA 128
QY 94 FDM-----MHSGPNKYM-LFGAACTHVTDFIAKSKWHHTQLSYADTHPMFTKDAF 144
Db 129 SDVKCANGDPPIFTKPKDKISGVIGAAASSYIMVANILRLFKIPQISYASTAPELSDNTR 188
QY 145 PNFF-RVWPSENAFNAPRLALKFENWTRVGTYYQNEPRYS-----LPHNHVADLDA 196
Db 189 YDFRSRVPPDSYQAQAMVDIVTALGNVYVSTL--ASEGNYGESGVFAFTQISREIGVCI 247
QY 197 MEVEVYETOSFVNDVAESLKLRE-KDVRILGNFNEHFARKAFCEAYKLDYMYGRAYOWL 255
Db 248 AQSQKIPREPRGCEFEKIIKLETPNARAVIMFANEDDIRLEAAKLNQSGH-FLWI 306
QY 256 IMATYSTDWNVTQDSECVSEETATALEGAILVDLLPLSTSGD-----ITVAGITAD 307
Db 307 -----GSDSGWGSKIAPVYQOEEIA---EGA--VTILPKRASIDGDFRYRSRTLANNRN 356
QY 308 EYLVEY-----DRL-RGTEYSRPHG---YTYDGIWAAALA 338
Db 357 VWFAEFEENFNGCKLGHGKRNSHIKCTGLERIANDSSEYQ-EGKVQFVIDAVYSWAYA 415
QY 339 IQYVAEKR-----EDLTHFDYRVKDWESVFLEALRNTSFEQVTG-PVR 381
Db 416 LHMHKERCPTYIGLCPRMWTIDGKELGY-----IRAVNFNSAGTPTVT 460
QY 382 F-YNNERKANILINQFOLQOME---KIGEYHSOKSHLDLS----- 417
Db 461 FNEGDAPGRYDIFYOYINNKSTEYKIIIGHTNQLHVKVEDMQWANREHTHPASVCSLPC 520
QY 418 -----LGKPKVKW-----VGKTPPKDRT-----LIVIE-H 440
Db 521 KGERKTKVKGPCWHCERCEGYNQVDELSCPLDQRPINRITGQRIPIIKLEWH 580
QY 441 SQVNPTIYVSASAVIGVIAFVFLAFNFIKYNQRYIKMSSPHLNNLIITVGCMITVLSI 500
Db 581 S-----PWAVVPVFIATLIIATTFVIVTFRYNDTPIVRASGRELSVLLTGIFLCY-SI 635
QY 501 IFGLDITLSSVAAPFYICTARAWILMAGFSLSFGAMFSKTRVHVHSIFTDKLN---KKV 557
Db 636 TELMI-----AAPDTIICSFRRIFGLGCMCFYSYAALLTKTNRIHRIFEQGGKSVAPKF 689
QY 558 IKDYQLFMVVGVLADIAIDIAITWQIADP-----FYRETKQLEPHENIDDLVIVPENE 612
Db 690 ISPASQLVITFSLISVQLLGVFVWFVDPPTIIDYGEQRTLDP-----ENARGV----- 740
QY 613 YCQSEHMTFVSIYAYKGLLVGAFIATWETRVHSIPALNDSKHIGFSVYVNFITCLAG 672
Db 741 KDISDLSLICSU--CYSILLMWTCTVYAIKTRGVF-ETFNEAKPIGFTWYTCIIWLAF 797
QY 673 AAISVLSDRKDLVFFV---LLSFFIIFCTATLCLVFPKLVKELKRNPGQVDRKVR--- 726

QY 350 LTHEDYRVKDNESVLEALRNTSPGVTPVRF-YNNERKANILINQFOLGOMEKIGETH 408
 Db 498 ---FNNYNTQTTDQIYRAMNSSSEGVSGHVYFDASGSRMAWTLTLEOLGGSKYKIGYYD 554
 QY 409 SOKSHDLDSLCKPVKWKCTPPKDRTLIYIEHSOVNPTIYIVSASASVIGIIVATVFLAF 468
 Db 555 STKD--DLSWKTDKWIGSGPPADOTLVKIFRFSQKLFISVSVLSSUGIIVLVVCLSF 612
 QY 469 NIKYRNORYIKMSPHLNLIIVGCMITYLISIFLGLDTLSSVAAFPYICTARAWILMA 528
 Db 613 NIYNSHRYIQNSQPNLNLNLAAGSLAAVFLGLDGYHGRNQFPVQCQARLWLLGL 672
 QY 529 GFSLSFGMSKTRWRVHSIFT---DLKLNKKVYKDYQLFMVVGVLADIALIITWQIAD 585
 Db 673 GFSLGYSMFTKIWWHTVFTKKEKKEWRKTLPEWPKLYATVGLLVGMDVLTLAIWQIYD 732
 QY 586 PFYRETKOLEPLHNEIDDLVIVPENECQSEHMTIFVSIYAYKGLLVLFQFAFLAWETR 645
 Db 733 PLHRTIETFAKEEPKEDIDVSLPOLEHCSSKMMTWLGIIFYGKGLLLGLLIGFLAYETK 792
 QY 646 HVSIPALNDSKHGFSVYVNVFETICLAGAAISLVLSDRKDLVFLVLSFFIETCTATCLV 705
 Db 793 SVSTEKINDHRAVGMAIYNVAVLCITAPVTMILSSQDAAFAFASLAIVFSYITLVVL 852
 QY 706 FVPKLVELKRNQGVVDRKVRATIRPMKNGRDRDSSVCELEQRDLRVKNTNCRFRKALME 765
 Db 853 FVPKMRRL--ITRGWQSEAOQTMKTGSSNTNNE-----BEKSRLLEKENELEKIIEA 904
 QY 766 KENELQALIRKL 777
 Db 905 KEERSVELRHLQ 916

RESULT 5
 GBRL_RAT STANDARD; PRT; 991 AA.
 AC Q92004; 008620; 008621; Q92308;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B RECEPTOR 1) (GABA-B-R1) (GB1).
 GN GABBR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
 RC STRAIN=RICO; TISSUE=Brain cortex, and Cerebellum;
 RX MEDLINE=9722131; PubMed=9069281;
 RA Kaupmann K., Huggel K., Heid J., Flor P.J., Bischoff S., Mickel S.J.,
 RA McMaster G., Angst C., Bittiger H., Froestl W., Bettler B.;
 RT "Expression cloning of GABA(B) receptors uncovers similarity to
 RT metabotropic glutamate receptors.";
 RL Nature 386:239-246(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1C AND 1D).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99092370; PubMed=9875211;
 RA Isomoto S., Kaibara M., Sakurai-Yamashita Y., Nagayama Y., Uezono Y.,
 RA Yano K., Taniyama K.;
 RT "Cloning and tissue distribution of novel splice variants of the rat
 RT GABAB receptor.";
 RL Biochem. Biophys. Res. Commun. 253:10-15(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1E).
 RC STRAIN=Wistar; TISSUE=Hippocampus;
 RX MEDLINE=99388283; PubMed=10457184;
 RA Pfaff T., Malitschek B., Kaupmann K., Prezeau L., Pin J.-P.,
 RA Bettler B., Karschin A.;
 RT "Alternative splicing generates a novel isoform of the rat

metabotropic GABA(B)R1 receptor.";
 Eur. J. Neurosci. 11:2874-2882(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1A), AND R1A-R2 INTERACTION.
 RC TISSUE=Brain;
 RX MEDLINE=99175124; PubMed=10075644;
 RA Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 RA Kargman S., Chateaufneuf A., Tsukamoto N., McDonald T., Whiting P.,
 RA Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 RA Bonner T.I., O'Neill G.P.;
 RT "Identification of a GABAB receptor subunit, gb2, required for
 RT functional GABAB receptor activity.";
 RL J. Biol. Chem. 274:7607-7610(1999).
 RN [5]
 RP TISSUE DISTRIBUTION.
 RX MEDLINE=20121644; PubMed=10658574;
 RA Belley M., Sullivan R., Reeves A., Evans J.F., O'Neill G.P.,
 RA Ng G.Y.K.;
 RT "Synthesis of the nanomolar photoaffinity GABA(B) receptor ligand CGP
 RT 71872 reveals diversity in the tissue distribution of GABA(B) receptor
 RT forms.";
 RL Bioorg. Med. Chem. 7:2697-2704(1999).
 RN [6]
 RP R1A-R2 INTERACTION.
 RX MEDLINE=99102694; PubMed=9872744;
 RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
 RA Kornau H.-C.;
 RT "Role of Heteromer Formation in GABA-B Receptor Function.";
 RL Science 283:74-77(1999).
 RN [7]
 RP MUTAGENESIS OF SER-247; SER-268 AND SER-269.
 RX MEDLINE=20159055; PubMed=10692480;
 RA Galvez T., Urwyler S., Prezeau L., Mosbacher J., Joly C.,
 RA Malitschek B., Heid J., Brabet I., Froestl W., Bettler B.,
 RA Kaupmann K., Pin J.-P.;
 RT "Ca(2+) requirement for high-affinity gamma-aminobutyric acid (GABA)
 RT binding at GABA(B) receptors: Involvement of serine 269 of the
 RT GABA(B)R1 subunit.";
 RL Mol. Pharmacol. 57:419-426(2000).
 CC -!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTINOCCEPTION.
 CC -!- COFACTOR: REQUIRES CALCIUM FOR HIGH AFFINITY BINDING TO GABA.
 CC -!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS: 1A, 1B, 1C, 1D AND 1E (SHOWN
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: ISOFORMS 1A, 1B AND 1C ARE EXPRESSED IN
 CC TESTIS, STOMACH, SPINAL CORD AND BRAIN INCLUDING CEREBRAL CORTICAL
 CC LAYERS, PYRAMIDAL CELL LAYERS OF THE HIPPOCAMPUS, GRANULAR CELL
 CC LAYERS OF THE DENTATE GYRUS, BASAL GANGLIA, CEREBELLUM
 CC (PREDOMINANTLY IN PURKINJE CELLS FOLLOWED BY GRANULAR LAYER).
 CC ISOFORM 1B IS ALSO EXPRESSED IN KIDNEY AND LIVER. ISOFORM 1D IS
 CC EXPRESSED IN FOREBRAIN, CEREBELLUM, EYE, KIDNEY, AND URINARY
 CC BLADDER.
 CC -!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 2. THE


```
Query Match      18.0%; Score 1156.5; DB 1; Length 960;
Best Local Similarity 32.7%; Pred. No. 1:1e-58;
Matches 259; Conservative 167; Mismatches 309; Indels 57; Gaps 16;

QY 18 WST-----ACGRT--AKRSVVYIAGFFPYGDCGVNSYTGKGVMPYVKLAGHVNHECKIL 70
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 149 WSTPKPCQVNRTPSERAVYIGALFPMGSGWPG---GQACQPAVEMAELEDVNSRRDIL 205
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 71 ANYRLHMWNDDTQCNAAYGVKSFDDMHSGPNKVMFLFGAACTHTVDPIAKSKHNLHTOL 130
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 206 PDYELKLTHSDSKCDPGQATKYLYELLYNDPIKIILM-PCGSSSVSTLVAAEARMNLIIVL 264
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 131 SYADTHP-MFTKDAPPNFRFVPSNAPNAPRALALKKFNTRVGTGVYVNEPRYSPLPHNH 189
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 265 SYGSSSPALSNRQPTPTFTHPSATLHNPTRVKLFKMGWKIATIQOTTEVFT----- 319
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 190 MVADLDAME-----VEVETQSFVNDVAESLKKLREKDVRIILGNFNEHFAKAFCEA 242
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 320 --SYLDDLEERVKEAGIEITFRQSFSDPAVPPVKLKRQDAIIIVGLFYETEARKEVCEV 377
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 243 YKLDMYGRAYQWLIMATYSTDMWNTQDS-EGSVBEIATALEGAILVDLLPLSTSGDITV 301
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 378 YKERLFGKKYWFELGWADNWKTYDPSINCTVEEMTEAVEGHITTEIVMLNPANTRSI 437
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 302 AGITADELYVEYDLRGTEYSRPHCY-----TYDGIWAAALAIQYVA-----EKREDL 349
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 438 SNMTSQEFVEKLTKRLKRHPETGFOEAPLAYDAIWAIALALALNKTSGGGSGRSGVRLED- 496
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 350 LTHFDYRVKDWESVFLALRNTSPFEGVGPVRF-YNNERKANILINOFOLGQWKEKIGEVH 408
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 497 ---FNNQTTDQIYRAWNSSFEGVSGHVVDASGRMAWTLIEQGGGYKKIGIYD 553
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 409 SOKSHLDLSLGPVKVWGKTPPKDRTLVIYIEHSQVNPTIYIVSASVIGCVIIATVFLAF 468
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 554 STKD--DLSWSEKTDKWIIGSPADQTLVKTFRFLSQKLFISVSVLSSGIYLAIVCLSF 611
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 469 NIKYRNQYIKMSPHLNLIIVGCMITVYLSIFIGLDTLSSVAAPFYICTARAWILMA 528
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 612 NIYNSHRYIQNSQPNLNLTAVGCSLAAVFLGLDGYHIGRSQFPPVQCQARLWLLGL 671
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 529 GFSLSGFAMFSKTRVHSHFT---DLKLNKKVQDYQYFVWVGVLADIALIITWQIAD 585
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 672 GFSLGYSMFTKIWMHVFTFKKEKWKRTLEPVMKLYATVGLVGMIDLAIWQIYD 731
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 586 PFYRETQLEPLHENIDVLVIPENEXQSEHMTIFVSIYAYKGLLVFGAFLAWETR 645
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 732 PLHRTIETFAKEEPKEDIDVSLPQLEHCSKKMTWLGIFYGKGLLLLLGIFLAYETK 791
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 646 HVSIPALNDSKHGFSVYVNFITCLAGAAISLVSDRKLDFVLLSFFIIFCTTATLCIV 705
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 792 SVSTEKINDHRAVGAIIYNAVLCITAPVTMILSSQQDAAFASALIVFSSYITLVVL 851
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 706 FVPKLVELKRNQGVVDRVRATLRPMKNGRRDSSVCELEORLDVKNTRCFRKALME 765
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 852 FVPKRRRL--ITRGWQSEADTMKTGSTNNNE-----EKSRLLEKENELEKIIAE 903
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
QY 766 KENELQALIRKL 777
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 904 KEERVELRHQL 915
   ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 4
GBR1 HUMAN STANDARD; PRT: 961 AA.
AC QUBS5; Q95375; Q90Q00; Q96022; Q95975; Q95468;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINO-BUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 1 PRECURSOR (GABA-B
DE RECEPTOR 1) (GABA-B-R1) (GB1).
GN GABBR1.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RC TISSUE=Cerebellum;
RX MEDLINE=99061981; PubMed=9844003;
RA Kaupmann K., Schuler V., Mosbacher J., Bischoff S., Bittiger H.,
RA Heid J., Froestl W., Leonhard S., Pfaff T., Karschin A., Bettler B.;
RT "Human gamma-aminobutyric acid type B receptors are differentially
RT expressed and regulate inwardly rectifying K+ channels.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14991-14996(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1A; 1B AND 1C).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872316;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Enson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor.";
RL Nature 396:679-682(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Brain;
RX Stroop U., Raming K.;
RT "Human mRNA for GABA-B1a receptor.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Fetal brain;
RX MEDLINE=98440782; PubMed=9753614;
RA Grifa A., Totaro A., Rommens J.M., Carella M., Roetto A., Borgato L.,
RA Zelante L., Gasparini P.;
RT "GABA (gamma-aminobutyric acid) neurotransmission: identification and
RT fine mapping of the human GABA(B) receptor gene.";
RL Biochem. Biophys. Res. Commun. 250:240-245(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=99014802; PubMed=9798068;
RA Goel V.L., Choi J., Ahn J., Bowles C.L., Raha-Chowdhury R.,
RA Gruen J.R.;
RT "Human gamma-aminobutyric acid B receptor gene: complementary DNA
RT cloning, expression, chromosomal location, and genomic organization.";
RL Biol. Psychiatry 44:659-666(1998).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1C).
RC TISSUE=Cerebellum;
RA Fraser N.J.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B), AND VARIANTS V-20 AND S-489.
RC TISSUE=Fetal brain;
RX MEDLINE=20184290; PubMed=9933300;
RA Peters H.C., Kaemmer G., Voiz A., Kaupmann K., Ziegler A., Bettler B.,
RA Epplen J.T., Sander T., Riess O.;
RT "Mapping, genomic structure, and polymorphisms of the human GABAB1
RT receptor gene: evaluation of its involvement in idiopathic
RT generalized epilepsy.";
RL Neurogenetics 2:47-54(1998).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).
RA Younger R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RC TISSUE=Cerebellum;
RX MEDLINE=99108069; PubMed=9889352;
RA Makoff A.;
RT "Molecular cloning of human GABAB1 and its tissue distribution.";
RL Brain Res. Mol. Brain Res. 64:137-140(1999).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM 1E).
RC TISSUE=Prostate;
```



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QY 173 VCTVQNEPRYSLPHNMVADLDAMEVEVETQSVDNDVAESLKKLREKDVRIILGNFNE 232
DB 198 VGLTQDVQRFSEVRNDLGVLYGEDIETSDTESFSDPCTSVKCLKGNVDVRIILGFQDQ 257
QY 233 HFARAFCAEYKLDYGRAYOWILMATYSFDWM- ---NVTQDSECSVEEITALEGAILY 288
DB 258 NNAKVFCCAYENMTGYSKIOWIIPGWYEPSWWEQVHTEANSSKCLRKNLLAAMEGYIGV 317
QY 289 DLLPLSTGSDIIVAGITADEYLVEYDLRL- GTEYSRFHGTYDYGIMAAALAIQVV- --- 342
DB 318 DFEPLSSKOIKTISGTPQOYERENKRSVGVPSKFGHAYDGIWIAKTQIORMETLH 377
QY 343 AKREDLLTHDYRVKDNESVFLAELRNSTFEGVTPVRYNNERKANILINPOLGOME 402
DB 378 ASSRHQRIQDFNYTDHGLRIILNAMNETNFFGVGTGVVFRNGERMCTIKFTQFQDSREV 437
QY 403 KIGEVHSOKSHLDLSLGGPKVWVGKTPPKDRTLIYIHSQVNTIYIVSASASVIGVIA 462
DB 438 KVGEYNAVADTLEI-INDTIRFOGSEPPKDKTIIELQRLKISLPSILSALTILGIMA 496
QY 463 TVFLAFNIKYRNQRYIKMSPHENLNIIVGCMITYILSIIFGLDITLSSVAAPFYICTAR 522
DB 497 SAFLPNIKNRQKLIKMSPPYNNLIIILGMSLSYASIFLFLDGSFVSEKTFETLCTVR 556
QY 523 AWILMAGFSLSGAMPKSTWRVHSIFTDLKLKKVIKDYQLFMVGVLLAIDIAIITWQ 582
DB 557 TWILTVGYTAFGAMFAKTWRVHAIFKNVKMKKKIIRKQKLLVIVGGMLLIDLCILCWQ 616
QY 583 IADPFYR-ETKQLEPLHNEID- ---DVLVIPENEVCQSEHMTIFVSIYAYKGLLLVF 636
DB 617 AVDPURRTVEKYSMEP- ---DPAGRDTSIRPLELHCENTHMTIWIIGVYAYKGLLLMF 670
QY 637 GAFLAWETHRVSPALNDSKHIGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLSFFLI 696
DB 671 GCFLAWETHRVSPALNDSKHIGFSVYVNFITCLAGAAISLVLSDRKDLVFLVLSFFLI 730
QY 697 CTTATLCLVFPKLVKELKNPOGVV-DKVRATLRPMKNGRRDSSVYCELEQ- ---RLRD 751
DB 731 CSTITLCLVFPKLVKELKNPOGVV-DKVRATLRPMKNGRRDSSVYCELEQ- ---RLRD 790
QY 752 VNTNCRFRKALMEKENELQALLRKL- ---GPEARKWIDGVCTGSGSVGSELEPIILNDIV 809
DB 791 LOSENHRLRMKITELDKDEEVTMQLQDTEKTYIK- ---QNHQELNDILN- --- 839
QY 810 RLSAPPVRREMPSTTVTMT-SVDSVTSTHVMDSNFSVQSTVMAPSLPPKKKQSIVE 868
DB 840 - ---LGNFTSTGDKKAILKHLNDQN- ---PQL- ---Q 865
QY 869 HHSAPAPTMQPIQO-QLQOHLQOHOQOQOHLQOQOHOQOQOQOHHHRLHLEKRN 927
DB 866 WNTTEPSRTCKPIEDINSPEHQRSLQLPIL- ---HHAYLPSIG 908
QY 928 SVSA 931
DB 909 GVDA 912

RESULT 2
GBR2_RAT STANDARD; PRT; 940 AA.
AC O88871; Q9QWU2; Q9JK36;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B
DE RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2).
GN GABBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

```

SEQUENCE FROM N.A.
TISSUE=Hypothalamus;

RC MEDLINE=99087320; PubMed=9872315;
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,
RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
RA Salom J.A., Morse K., Laz T., Smith K.E., Nagarathnam D., Noble S.A.,
RA Branchek T.A., Gerald C.;
RT "GABA(B) receptors function as a heteromeric assembly of the subunits
RT GABA(B)R1 and GABA(B)R2.";
RL Nature 396:674-679(1998).

[2]

SEQUENCE FROM N.A.

RC TISSUE=Brain cortex, and Cerebellum;
RX MEDLINE=99087322; PubMed=9872317;
RA Kaufmann K., Malitschek B., Schuler V., Heid J., Froestl W., Beck P.,
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
RA Bettler B.;
RT "GABA-B receptor subtypes assemble into functional heteromeric
RT complexes.";
RL Nature 396:683-687(1998).

[3]

SEQUENCE FROM N.A.

RC TISSUE=Brain cortex;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL Brain Res. 860:41-52(2000).

[4]

SEQUENCE FROM N.A.

RC TISSUE=Hypothalamus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

[5]

RIA-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.

TISSUE=Hippocampus;

MEDLINE=99102694; PubMed=9872744;

Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,

Kornau H.-C.;

"Role of the Receptor Formation in GABA-B Receptor Function.";

Science 283:74-77(1999).

-!- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
ANTINOCICEPTION.

-!- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
HAPPEN.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER

COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A

PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE

PLASMA MEMBRANE.

-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
HABENULA, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
CEREBELLUM.

-!- DEVELOPMENTAL STAGE: ABUNDANT IN BRAIN CORTEX AND CEREBELLUM
THROUGHOUT POSTNATAL DEVELOPMENT WHEREAS ITS EXPRESSION IN SPINAL
CORD GRADUALLY DECREASES.

-!- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.

-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.

GABA-B RECEPTOR SUBFAMILY.

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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:04:53 ; Search time 24.07 Seconds
(without alignments)
1858.375 Million cell updates/sec

Title: US-09-715-962-4

Perfect score: 6409

Sequence: 1 MFRPSWPFASLLFLLLWST.....SAVGSCNPISIKCDIVEYL 1220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36564827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1598	24.9	941	1	GBR2_HUMAN
2	1578.5	24.6	940	1	GBR2_RAT
3	1156.5	18.0	960	1	GBR1_MOUSE
4	1151.5	18.0	961	1	GBR1_HUMAN
5	1134	17.7	991	1	GBR1_RAT
6	316	4.9	908	1	MGR8_RAT
7	312	4.9	908	1	MGR8_HUMAN
8	309	4.8	912	1	MGR4_RAT
9	305	4.8	908	1	MGR6_MOUSE
10	305	4.8	912	1	MGR4_HUMAN
11	289.5	4.5	976	1	MGR_DROME
12	286.5	4.5	915	1	MGR7_HUMAN
13	280.5	4.4	915	1	MGR7_RAT
14	278.5	4.3	1212	1	MGR5_HUMAN
15	276.5	4.3	1194	1	MGR1_HUMAN
16	271.5	4.2	1079	1	CASR_MOUSE
17	268	4.2	877	1	MGR6_HUMAN
18	268	4.2	1203	1	MGR5_RAT
19	265.5	4.1	1079	1	CASR_RAT
20	261.5	4.1	1199	1	MGR1_RAT
21	258.5	4.0	871	1	MGR6_RAT
22	256	4.0	1078	1	CASR_HUMAN
23	246	3.8	872	1	MGR2_RAT
24	246	3.8	879	1	MGR3_RAT
25	237.5	3.7	999	1	MGR1_CAEEL
26	231	3.6	877	1	MGR3_HUMAN
27	229	3.6	1085	1	CASR_BOVIN
28	226	3.5	872	1	MGR2_HUMAN
29	211	3.3	550	1	CCF_DROME
30	199.5	3.1	540	1	ANPC_HUMAN
31	196.5	3.1	708	1	GBF_DICDI
32	196	3.1	1231	1	YKT3_CAEEL
33	195	3.0	537	1	ANPC_BOVIN

RESULT 1

ID	GBR2_HUMAN	STANDARD:	PRT:	941 AA.
AC	075899; 075974; 075975; Q9UNR1; Q9PIR2;			
DT	20-AUG-2001 (Rel. 40, Created)			
DT	20-AUG-2001 (Rel. 40, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2 PRECURSOR (GABA-B RECEPTOR 2) (GABA-B-R2) (GB2) (GABABR2) (G PROTEIN-COUPLED RECEPTOR 51) (GPR 51) (HG20).			
GN	GABBR2 OR GPR51.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RP	SEQUENCE FROM N.A. (ISOFORM 2A).			
RC	TISSUE=Cerebellum;			
RX	MEDLINE=99087321; PubMed=9872316;			
RA	White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H., Barnes A.A., Emson P., Foord S.M., Marshall F.H.;			
RT	"Heterodimerization is required for the formation of a functional GABA(B) receptor."			
RL	Nature 396:679-682(1998).			
RN	[2]			
RP	PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).			
RC	TISSUE=Brain;			
RX	MEDLINE=20193514; PubMed=10727622;			
RA	Clark J.A., Mezey E., Lam A.S., Bonner T.I.;			
RT	"Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";			
RL	Brain Res. 860:41-52(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2A).			
RA	Liu M., Parker R., McCrean K., Watson J., Baker E., Sutherland G., Herzog H.;			
RT	"Cloning and characterization of a novel human GABA-B receptor subtype with high affinity for GABA and low affinity for baclofen.";			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2A).			
RC	TISSUE=Hippocampus;			
RA	Borowsky B., Laz T., Gerald C.;			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 2A).			
RC	TISSUE=Fetal brain;			
RX	MEDLINE=99189236; PubMed=10087195;			
RA	Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P., Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F., O'Neill G.P., Liu Q.;			
RT	"Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB receptors expressed predominantly in nervous tissues and mapped proximal to the hereditary sensory neuropathy type 1 locus on chromosome 9.";			
RL	Genomics 56:288-295(1999).			
RN	[6]			

ALIGNMENTS

DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SQ SEQUENCE 983 AA; 109276 MW; 072F0DB83A840A80 CRC64;

Query Match		4.4%	Score 281;	DB 11;	Length 983;
Best Local Similarity		20.0%	Pred. No. 1.9e-11;		
Matches 171; Conservative 147; Mismatches 303; Indels 234; Gaps 38;					
QY	30	DVYIAGFP-YGDGVENSYTG-----RGV--MPSVKLALGHVNEHGKILANRYLRHMMWND	81		
Db	48	DITLGLFPVHGRGSEKACGELKKEAGIHRLEAMLFALDRINNDPDLIPNITIGARILD	107		
QY	82	TQCN-----AAGVKVSFDM-----MHSGPNKM-LFGAACTHVTDP	119		
Db	108	T-CSDTHALEQSLTFVRALIEKDGTVEKCGSGGPPITKPERVGVIGASGSSVIMVA	166		
QY	120	KASKHHLTQLSYADTHPMETKDAFPNFF-RVVPSENAFNAPRLALLKEFNWTRVGT	178		
Db	167	NILRLFKIPQISYASTAPDSNRYDFFSRVPSPDYQAQAMVDIVRALKNYVSTL-A	225		
QY	179	NEPRYSLPHNHVADLDAMEVEVVEVETQSFVND---VAESLKKLRE-----	220		
Db	226	SEGSYG-----ESGVEAFIQKRENGGVCIAGSVKIPREPKTGEFDKIIKRLLE	274		
QY	221	-KDVRIILGNFNEHFAKFACEAYKLDIMYGRAYQWLIMATYSTDMNVTQDSECSVEE	279		
Db	275	TSNARGIIIFANEDDIRVLEAARRANQTGHFF-WM-----GSDSWGSKSAPVLRLE	328		
QY	280	TALEGAILVDLLPLSTSG-----DITVAGITADEYLVEYDR---LRGT	321		
Db	329	---EGAVTILPKRMSVRGFDYFSRTLDNNRNINWFAEFWEDNFHCKLSRHALKKGSH	385		
QY	322	SREPHG-----YTDGIWAAALAIQYVAEKREDLLTHFDY-----	355		
Db	386	KKCTNRERICQDSAYEQEGKVQFVIDAVYAMGHALHAM-----HRDLCPRGVGLCP	436		
QY	356	RVKDWESV-FLEALRNTSFEQVTG-PVRF-YNNERKANILINPOL---GOMEKIGEYH	408		
Db	437	RMDPVDGTQLLKVIYRNFNFSIAGNPVTFNENGDPAGRYDIYQOLRNGSAEYKVIG---	493		
QY	409	SQKSHLDLSLGKPKVWVG-----	426		
Db	494	SWTDHLHLRIER-MQWPGSGQQLPSICLPCQGERKKTVMGMACCWHPCECTGYQYQV	552		
QY	427	-----KT-----PPKDRTL---IYIEHSQVNPITYIVSASVIGVLIATVFLAFN-IK	471		
Db	553	DRYCKTCPYDMRTERNTSCQPIPIVKLEWDSWAVLPLFLAVVG-IAATLFVVVTFVR	611		
QY	472	YRNORYIKMSSPHLNLIIVGCMITYLSIIFGLDITLSSVAAFPYICTARAWILMAGFS	531		
Db	612	YNDTPIVKASGRELSYVLLAGIFLCYATTFMLIAEPDLGT-----CSLRIFLGLGMS	664		
QY	532	LSFGAMFSKTRVHISITDULKN---KKVIKDYQLFMVGVLLAIDIAITWQIADPF-	587		
Db	665	ISYAALITKTNRIYRIFEOGKRVSAPRFPASQALAITFILISLQLLGICWVFWDP	724		
QY	588	-----YRETKOLEPLHHE-----NIDDLVIVPENECQSEHMTIFVSIYAYKGLLVGA	638		
Db	725	SVVDFODQRTLDRFARGVLKDCISLSLI-----CLLGYSMLLMVTCT	768		
QY	639	FLAWETRHVSIPALNDSKHIGFSVYNNVFTCLAGAAISLVLSDRKDLVFN---LLSFFII	695		
Db	769	VYAIKTRGVF-EYFNEAKPIGFTMYTCIWLAFIPFFGTISQSADKLYIQTTTLTVSVS	827		
QY	696	FCTATLCLVFPKL	710		
Db	828	LSASVSLGMLYMPKV	842		

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BERKELEY;
RX  MEDLINE=20196006; PubMed=10731132;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Fostier C., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA  Frazier C., Garg N.S., Gelbart W.M., Glasser K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Mourtulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svrtk R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
DR  EMBL; AE003846; AAF59402.1; -.
DR  FlyBase; FBgn0019985; Glu.RA.
DR  InterPro; IPR001828; ANF_receptor.
DR  InterPro; IPR000337; GPCR_Mgr.
DR  Pfam; PF00003; 7tm_3; 1.
DR  Pfam; PF01094; ANF_receptor; 1.
DR  PRINTS; PR00248; GPCRMR.
DR  PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR  PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR  PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR  PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SQ  SEQUENCE 976 AA; 108485 MW; 43A0E1F918EDACC4 CRC64;

Query Match 4.5%; Score 285.5; DB 5; Length 976;
Best Local Similarity 19.2%; Pred. No. 8.9e-12;
Matches 171; Conservative 130; Mismatches 345; Indels 245; Gaps 31;

QY 30 DVYIAGFFPYGDGVNSYTG-----RGV--MPSVKYKALGHVNEHGKILANRLHWMNDT 82
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44 DIILGLFPVHEKGEAPCPKPVKVRQORLEAMLYAIDRVNNDPNILPGITIGVHILDT 103
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 QCNAAGVCKSFDDMMISGPNKVMFLGGAACHTVDP----- 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
104 CSRDTYALNQSLQFVFRASLNNLDTSGYECADGSSPQLRKNASSGPFVGVIGGSSVSLQ 163
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
118 IAKASHKHHLTQLSYADT-HPMTTKDAFPNFRVVPSPENAFNAPRALLLKEFNTRGVCTV 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
164 VANLLRLFLHPQVSPASTAKTLSDKTRFDLFARTVPDPTQTSVALVLLKFNFNWSYVSTI 223
QY : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177 YQ--NEPRYSPLPHNHMVADLDAMEVEVVE-----TQSFVNDVAESLKK-----L 218
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Db 811 SVLSATVALGCMFVKKVYIIILAKP-----ERNVRSFTTSTVVRMHVGDGKSSSAASRS 866
Qy 741 SVCELEQLRDKVNTNCRFR-KALMEKENELQALIRK-LGPEAR-----KWID 786
Db 867 SLVNLWKR-RGSSGETLRYKGRRLAPHKSEIECTPKGSMGNGRATWTSSNGKSVSMAQ 925
Qy 787 GVTCTGSGNVSLEPIINDIVLSAPVVRREMPSTVTMTSVDSTVSTHVMDSNFV 846
Db 926 NEKSSRGHLWQLRSLIHIN-----KKENPNQTA-----954
Qy 847 SVQSTVMAPSLPPKKKKSIVIEHHSHAP-----TMMQPIOOLOLQHOQHOQOQHLQ 902
Db 955 -----IKPFSKSTDSRRHSSATFPETSAKTLVDVSAEQYPAQYRPPQSPIS 1004
Qy 903 QOQHQQOQOQOQOQHHRHLEKRNVSQAOTDDNIGTSITAGKRGSGDCSMRMRROST 962
Db 1005 TVSH-----RTASVSRTEDDAPTQSEPPQSRSSSQSLMEQISSV 1045
Qy 963 ASRHYDSGQPTTARPKYSSSHRNSSTNISTQSLSNMCPSKSTPAVTKPTASDHR 1022
Db 1046 VTRF-----TANI-----SELNSK-----MLSTATPG--- 1067
Qy 1023 RTSMGSALKSNFVYSQSLDWTHTLSHAKQSQSPR---NYASPORCAEHGG--HGMYYD 1077
Db 1068 -TWATPLCSSYLLPREIQTLPMTTFAEIQLPLPSIEVNGASQARKOSNGSVKEGTAPT 1126
Qy 1078 PNTTSPIQRSYSEKRNKRHPKQKGTVCQSETDSE 1113
Db 1127 PSAQODLELVALPPSPFRSDIDSGSASPSPVSE 1162

RESULT 12
Q98UC4
ID Q98UC4 PRELIMINARY; PRT; 1242 AA.
AC Q98UC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICED VARIANT F.
GN MGLR5F.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA StorzJohann L.L., Stormann T.M., Parks T.N.;
RT "Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227203; AAK01488.1; -.
KW Receptor.
SQ SEQUENCE 1242 AA; 138063 MW; 9ED84AFEFA2CF0EB CRC64;

Query Match 4.78; Score 303; DB 13; Length 1242;
Best Local Similarity 18.98; Pred. No. 7e-13;
Matches 260; Conservative 204; Mismatches 471; Indels 442; Gaps 61;

Qy 12 LFLFULLSTACGR-----TAKR-----SDVYIAGFF-----PYGDGVENSYTKR- 50
Db 7 LAIILLKEDVCGNFGLLVSAQANERRVVAHMPGDIIGALFSVHHQPIVDKVRHKCGEV 66
Qy 51 ---GV---MPSVKLALGHVNEHGHKILANYRLHMMWMDTQCNAAGVKGFFDM-----97
Db 67 REQYGIQRVEAMLTDLRINDPLTLLPNITLGCIEDRDCSWHSAVALEQSIIEFIRDSLSS 126
Qy 98 -----HSGPNKYNLFGAACTHYVDPTAKAKSHWHLTQLSYADTH-PMF 139
Db 127 EEEGMYRCVDGSSSFHSSKRPVIGVPGSSVAIQVONLLQLFNIPQIAYSATSMDSLS 186
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Qy 140 TKDAPFNFRVVPSENAFNAPRLALLKEFNWTRVGVYQNEPRYSLPHNHMVAIDLAME- 198
Db 187 DKTFLKFMVVPDQAQARAMVDIVKRYNWTIVYSAVH-TEGNYGSGMEAFKDMAKEG 245
Qy 199 VEVVETQSFVNDVAES-----LKKLRE--KDVRIILIGNFNEHFARKAFCAYKLDYMGRA 251
Db 246 ICIAHSYKITYSNAGEOSFKLLKRLKSLHPKARV-----ACFCE-----GMT 288
Qy 252 YOWLMATYSTDWNVNTQDSECSVEIATALEGAILLDLPLSTSG-----DIT-----300
Db 289 VGLLMA-----MRLGLAGE-----FLLCGSDWADRYDVTGYQRE 326
Qy 301 -VAGITA-----DEYVEYD-----RLRG--TEYSRFH-- 325
Db 327 AVGGITIKLQSPDKWFDYILELRPETNHRNPFQEFQWHRFOCRLEGFPPOENPKYNT 386
Qy 326 -----GTYDGIWAAALAIQ-----YVAEKREDLLTHFYDVRKD 359
Db 387 CTSQMTLRTQHVQDSKMGFVINAIYSMAYLHNMQLSLCPGYVG--LCDAMKPIDGR---441
Qy 360 WESVFLAALRNTSFEGVTGPVRFYNNERKANILINOFOLGOMEKIG-----405
Db 442 ---KLLSLMKNTFTGVSQDMLFDENGSP---GRYEIMNFKMKGKDYFDYINVGSWDN 495
Qy 406 -----EYHSQKSHLDLSL-GKP-----VKWVGK-----TPPKDRTLIIYIEHS- 441
Db 496 GELKMDDEIWESEKNIIIRSCVCEPCKEKGQIKVIRKGEVSCCWTCTPCKENEVVFEYTC 555
Qy 442 -----QVNPITYIVSASASVIGVII-----ATVFL-AFNIKYRNQRY 477
Db 556 KACQLGSPNDELTCGDLLIPVQVLRMGDPEPIAAVYFACGLGLATLFTVAIFIMYRDTVP 615
Qy 478 IRKMSPHLNLNLIIVG-----CMIT-----YLSIIFGLDITLSSVAAPFICTA 521
Db 616 VKSSRELCTYIILAGICLGLCTFCLIAKPOQIYCLQIGIGLSP-----661
Qy 522 RAWILMAGFSLSGFAMFSKTRVHSIFTDLKLNKKVIKDYQLFM-----VVGVLIAID 574
Db 662 -----AMSYALVTKTNRILARLAGSK--KKICTKKPRMSACAQVIAFILICIQ 710
Qy 575 IAIITWQIADPFYRETKOLEPLH-HENTDDVLVIPENECYCOSEHMTIFSVIYAKGLL 633
Db 711 LGIIVLALFTMEP-----PDIIMHDYPSIREVYLI-----CNTNLGVVYVTP--GYNGLL 756
Qy 634 LVYGAFLAWETRHSVIPA-LNDSKHIGFSVYNVFTCLAGAAISLVLSRKDLVFLVLSF 692
Db 757 ILSCIFYAFKTRNV--PANFNEAKYIATFTYTTITWLAFFVPIYF-----GSNYKIITMCF 810
Qy 693 FTIFCTTATCLVFPVKLVKLVRNPGQVVDKRVRAFTR-----PMKSKNGRRDS 740
Db 811 SVLSATVALGCMFVKKVYIIILAKP---ERNVRSFTTSTVVRMHVGDGKSSSAASRS 866
Qy 741 SVCELEQLRDKVNTNCRFR-KALMEKENELQALIRKLGPEARKWIDTCTGCGSNVGE 799
Db 867 SLVNLWKR-RGSSGETLRYKGRRLAPHKSEIECTPK-----GSMGNGGRATMTS 915
Qy 800 LEPILNDDIVRLSAPVVRREMPSTVTMTSVDSTVSTHVMDSNFVSQSTVMAPSLPP 859
Db 916 EESVCIPECNRSESSRDEKEVP-----VKEDALTG-----945
Qy 860 KKKKSIVIEHHSHAPAPTMQPIQOOLQHOQHOQOQOQOQOQOQOQOQOQOQOQH 919
Db 946 -KKTGNCV-----SLIVPQDCQLDLKHS--NGKSVSWAGNEKSSRGHLWQLR 993
Qy 920 HRHLEKRN-----VSAQTDNIGSITAGKRSRG--DCSSMRER-----958
Db 994 SIHINKENPNQTAIVKIPFSKSTDSRRHSSATFPETSAKTLVDVSAEQYPAQYRPT 1053
Qy 959 -----RQSTASRHYDSGQPTTARPKYSSSHRNS-----STNISTQSLSN 1001
Db 1054 PSPSTVSHRTASVSRTEDDAPTQSEPPQSRSSSQSLMEQISSVVTFTANISELSNM 1113
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QY 694 IIFCTTATLCLVFPVKLVKLRNPOGVVDKRVATLRPMKNG-----RRDSS-----V 742
Db 392 FLIGTTMIIGLVFVRMVGLYDPQG-----DNIKISNSHGSHVPRDRDSAYSPDAEI 444
QY 743 CELEQRDRVK 753
Db 445 RRLKQRISELE 455

RESULT 10
Q90Y85 PRELIMINARY; PRT; 153 AA.
AC Q90Y85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GABA-B RECEPTOR 2 (FRAGMENT).
GN GABABR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE=99263199; PubMed=10328880;
RA Martin S.C., Russek S.J., Farb D.H.;
RT "Molecular identification of the human GABABR2: cell surface of
RT expression and coupling to adenylyl cyclase in the absence of
RT GABABR1."
RL Mol. Cell. Neurosci. 13:180-191(1999).
DR EMBL; AF112975; AAF18937.1; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 153
FT NON_TER 153
SQ SEQUENCE 153 AA; 17211 MW; 4335487AAFI23D6C CRC64;

Query Match 5.1%; Score 329.5; DB 11; Length 153;
Best Local Similarity 41.2%; Pred. No. 3.1e-16;
Matches 63; Conservative 37; Mismatches 52; Indels 1; Gaps 1;

QY 384 NNERKANILINPOLGOMEKIGYHSOKSHLDSLGLKPKVKGKTPKDRTLIYHSQV 443
Db 2 NGERMGTIKFTQDSREKVGEYNVADTLEI-INDTIRFOGSEPKDKTILEQLRKI 60
QY 444 NPTIYVSASVIGVIATVFLAFNFKYENQYIKMSSPHLNLIIIVGCMITVLSIFL 503
Db 61 SLPYLSALTILGIMIMASAFLEFNKRNQKLIKMSSPYMNLIILGGMLSYASIFL 120
QY 504 GLDTTLLSVAAPFYICTARAWILMAGFSLSFGA 536
Db 121 GLDGSFVSEKTFETLCTVTRTILTVGYTTAFGA 153

RESULT 11
Q98UC5 PRELIMINARY; PRT; 1188 AA.
AC Q98UC5;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE RECEPTOR 5 SPLICE VARIANT B.
GN MGLUR5B.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=BRAIN;
RA Storjohann L.L., Stormann T.M., Parks T.N.;
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RT "Molecular Cloning and Functional Expression of Chick Metabotropic
RT Glutamate Receptor 5 Splice Variants.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227202; AAK01487.1; -.
KW Receptor.
SQ SEQUENCE 1188 AA; 132053 MW; 6C179BF8C8045BBD CRC64;

Query Match 4.7%; Score 304; DB 13; Length 1188;
Best Local Similarity 18.4%; Pred. No. 5.5e-13;
Matches 250; Conservative 199; Mismatches 453; Indels 454; Gaps 60;

QY 12 LFLLLMSTACGR-----TAKR-----SDVIAGFF-----PYGDGVENSYTGR- 50
Db 7 LAILLKEDVCGNFGLLVSAQANRRVVAHMPGDIIGALFVHHQPTVDKVKHERKCEV 66
QY 51 ----CV--MPSVKLALGHVNEHGKILANVRLHWMNDTQCNAAVGVKSEFFDM- 97
Db 67 REQYGIORVEAMLHTLDRLNDPTLLPNITLGCETRDSCHWSAVALDEQSIEFIRDLISS 126
QY 98 -----HSGPNKVMLFCAACTHTVDTPIAKASKKHWHLTQLSYADTH-PMF 139
Db 127 EEEEGMVRCDVSSSPHSHKPIVGVICGSSSVAIQVONLLQLENIPQAIYSATSMDS 186
QY 140 TKDAPPNFRVVPSENAFNAFLALLKEFNWTRVGTVYQNEPRYSLPHNHMVADLDAME- 198
Db 187 DKTLFKYFMRVVPDQAQARAWDIVKRYNWTYVSAVH-TEGNYGESGMEAFKDMAKEG 245
QY 199 VEVVETQSFVNDVAES-----LKKLRE--KDVRIILGNFNEHFARKACEAYKLDMYGRA 251
Db 246 ICIAHSYKIYSNAGEQSFDKLLRLKRLSHLPKRVV-----ACFCE-----GMT 288
QY 252 YQWLIMATYSTDWNVTQDSECSVEEATALEGATLVLLPLSTSG-----DIT----- 300
Db 289 VRGLMA-----MRRUGLAGE-----FLLGSDGWADRDVDTGYORE 326
QY 301 -VAGITA-----DEYLVEDY-----RLRG--TEYSRFF-- 325
Db 327 AVGGITIKLQSPDKWKFDDYVLELRPETNHRNPWFQEFWQHRFCRLEGFPOENPKYNT 386
QY 326 -----GYTDGIWAALATQ-----YVAEKREDLLTHFYRVKD 359
Db 387 CTSQMTLRTQHVQDSKMGFVNAIYSMAVGLHNMOLSLCPGVG--LCDAMKPIDGR--- 441
QY 360 WESVFLRALRNTSEFVGTGVPVRFYNNERKANILINQFOLGOMEKIG----- 405
Db 442 ---KLLESMTNTFGVSGDMILFDENGDS-GRYEIMNFKKMGKDYFYINVGSDN 495
QY 406 -----EYHSQKSHLDSL-GKP-----VKWVGK-----TPPKDRFLIYIEHS- 441
Db 496 GELKMDDEIWSEKNNIIRSCPECKGQIKVIRKGEVSCCWTCTPCKENEYVFDEYTC 555
QY 442 -----QVNPTIYVSASASVIGVI-----ATVFL-AFNIKRYNORY 477
Db 556 KACQLGSPNDELTCGLIPVQYLRWGDPEPIAAVVFACLGLLATLFTAIPIYRDPV 615
QY 478 IKMSSPHLNLIIVG-----CMIT-----YLSIFLGLDITLSSVAAPFYICTA 521
Db 616 VKSSRELCTIILAGICIGYLCCTFCLIAKPOQIYCYLQIRIGLSP----- 661
QY 522 RAWILMAGFSLSFGAMFSKTRWRVHSIFTDLKLNNKVIKDYQLFM-----VVGVLAI 574
Db 662 -----AMSYSALVTKTNRIRIARLAGSK--KKICTYKPFPMSCAQLVAFILICIQ 710
QY 575 IAITTTWQIADFFVRETKOLEPLH-HENIDDLVLTIPENEYCOSEHMTIFVSIYAYKGL 633
Db 711 LGIIVALTIMEP-----PDIMHDYPSIREVYLI-----CNTNLGVVTP- 756
QY 634 LVFGAFLAWETHRSIPA-LNDSKHIGFSVYNNVFTCLAGAAISLVSDRKLDFVLSF 692
Db 757 ILSCTFYAFKTRNV--PANFNEAKYIAFTMTCTCIWLAFVFIYF-----GSNYKITMCF 810
QY 693 FIIFCTTATLCLVFPVKLVKLRNPOGVVDKRVATLR-----PMKNGRRDS 740
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Db 330 TVEDLENRCMEAGVEIVTROSLSDPTDAVRNLRQDARIIVGLFVYVVAARRVLCMEYKQ 389
QY 246 DMYGRAYOWIMATYSDWNVTQDSE---CSVBEIATALEGAILVDLLPLSTGSDIIVA 302
Db 390 QLYGRAHWFFIWNWYENVLKAEGITVEQMRIAABEGHLLTTEALMNNQNTTIS 449
QY 303 GITADEY---LVEYDRLR-----GTEYSRE-HGY-----TYD 330
Db 450 GMTAAEERLVLVLLPLKFLLOCAFFLRRLHNLQALIEEGYDINHRYPEGQEAPLAYD 509
QY 331 GIWAAALAIQVAEK---REDLLTHFDYRVKDWESVFLEALRNTSFEGVTGPVRYN-NE 386
Db 510 AVMSVALAFNKTMBRLTGTGKSLRDFYTDKEIADEIYAANNSTQFLVSGVWAFSSOGD 569
QY 387 KANILINQFOLGOMKIGEVHSHQSHLDLSLGPVKVWG----- 426
Db 570 RIALTOEQMIDGKYEKLYGYDTQLD--NLSWLNTEQWIGGKTKHVHTPEPNKGNPSKD 627
QY 427 -----KTPPK----- 431
Db 628 DVNTRGSLTSLSEKNDESKNPSSASLQAPKVPKPKKLSISDAGKDTVTQVKENEPEP 687
QY 432 ----- 431
Db 688 GFSQOFKESIGVRANRNSSATKKENEKLLVTVPGKSLIKESNDENVPSRRTKSQPVG 747
QY 432 ----- 431
Db 748 KKYVEESSTRVREPFDSDREKYLSMDIDYDRSSEDEVPEKLSWEPDSTLRRRVSNNE 807
QY 432 ----- 431
Db 808 YHSSLEGEERIDDSVGSSTMRGSRYPQNAEDERPVIILAEIINMGKIKELKEQRESTN 867
QY 432 -----YIVSAS-----ASV--IGVLIATVFLA 467
Db 868 VFRNRRDDKTIDEVSGSKITGTSKQHVEEVKYNETASNEDDQNAQVXHGIFITKIFSA 927
QY 468 FNIK----- 471
Db 928 QRMKEKSSKESEEDENKDKVKKDENKDEQKLPPEPELEAKKAWFPPIAETSPD 987
QY 472 -----YRNORY----- 477
Db 988 IPGENQILQYQVKIGKRNKRYCIGINTDISRKSKITKTFKSAGDDL VVYHDGRLR 1047
QY 478 ----- 477
Db 1048 DIGOTTENLKNQRNHHKHTPEDDIPVDIGHSDDRVREIGVNTKKLPKIIIPPIAEMVH 1107
QY 478 -----IKMSPHLNNLI----- 490
Db 1108 KNGKLRIIGTSDKFPWPDIDGTDVIYMHPIKTDKRLKLNKLIVDPDPPDNGPVKMPKTEDR 1167
QY 491 -----VGCMTY-----LSIFIGLDTFLSSVAAF 515
Db 1168 RYYKGCYHPGRTWRRLFFNFKYLRKRRPSHWLYTLVFSVLYI-LFVILFMAWF 1226
QY 516 PYI----- 518
Db 1227 DFIKDDASRKVPIMKMAQPFISFTPIGPRTNPKAVSFDPRNSTEYMEKYAGIMALLEKYG 1286
QY 519 -----CTARAWI-----LMAGF-----SLSFAM 537
Db 1287 DYGNPRGTCANEKGYPSGEPVFLKNRIIGFKTEPIYNSDELVKAKIDEVEFTAL 1346
QY 538 -----FSKTW-----RVHSIFTD----- 550
Db 1347 KRLENTTTEBGLNRTWITCRSDKDNVLFTEHPEPAIRTEYTDIEEKIEYIANEGKKS 1406
QY 551 -----LKNKK-----VIKDYQLPMV-----GVLLAID 574
Db 1407 FFGPNVNRIVALKIKNLKANERVHINCKIVIOSSHVPNCNTIMLFGVILICLSVILLGD 1466
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QY 575 IAIITWQ---IADPF--YRETKOLE-PLHHENIDDLVIPENEYCOSEHMTIFVSIYA 628
Db 1467 GRFVSPEEYKPFDPQLORYLETFPLEDPV--STDDDIKIRPELEHESORNMMGLVYG 1524
QY 629 YKGLLIVFCALAWETRHSVIPALNDSKHIGFSVNVFITCLAGAAISLVLSDRKDLV 688
Db 1525 FKLILVFLFLAYETRSIKVQINDSRVGVSIYVNVVLCLITAPVGVIAQQDASFA 1584
QY 689 LLSFFIIFCTATLCLVFPVKLVKLRNPQGVVDKRVKTRATLRPMKSNGRDSSVC-ELEQ 747
Db 1585 EVALAVIFCCFLSMLLIFVPKVIEVRHPKDKAESKYNP-----DSAISKEDEE 1633
QY 748 RLRDVKNTCNCRFKALMEKENELQALIRKL---GPPARKWIDGVTCTGGSNVGSELEP 802
Db 1634 RYQKLVTENEELQRLTOKEEKIRVLRQRLVERGDAGKTELNGATGVASAAVATTQSP 1691
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RESULT 9

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O96954
ID O96954 PRELIMINARY; PRT; 528 AA.
AC O96954;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE METABOTROPIC GLUTAMATE GABA-LIKE RECEPTOR.
GN MGRL.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Astrophorida; Geodiidae; Geodia.
OX NCBI_taxid=6047;
RN [1]
RP SEQUENCE FROM N.A.
RA Perovic S., Prokic I., Krasko A., Mueller I.M., Mueller W.E.G.;
RT "Origin of neuronal receptors in Metazoa: cloning of a metabotropic
RT glutamate/-like receptor from the marine sponge Geodia cydonium.";
RL Cell Tissue Res. 0:0-0(0).
DR EMBL; Y17211; CAA76688.1; -.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
DR ProSite; PS50259; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 528 AA; 58641 MW; 0B99D8357FEAB31 CRC64;
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Query Match 6.5%; Score 418; DB 5; Length 528;
Best Local Similarity 29.2%; Pred. No. 8.6e-22;
Matches 126; Conservative 90; Mismatches 163; Indels 52; Gaps 14;

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QY 362 SVFLEA-----LRNTSPGVTGPVRFYNNE--RKANTL-INQFOLGOME----KIGEVHSQ 410
Db 38 SVFERMFQHLQNTSPAGLSGKTVQFDEGIREINVLDMVQYQWNNSEIDRVIVGETRVE 97
QY 411 KSHL-----DLSLCKPVKVGKTPPKDRPLIYIEH-SQVNTPIYIVSASVIGVIAIV 464
Db 98 ESLVTHYLPFPFHENPMPDGPDPNDG---IPIENVTVSVPLTVVYVALAGGLFAIV 154
QY 465 ELAFNKKYRNORYKMSPHLNNLIIVGCMITVLSIFLGLDTLSSVAAPFYICTARAW 524
Db 155 CVFTTVIFKRKLIRUSSPNLNLIGLGAIIYFNVTILVPTTDDVIAAI--LCNINPW 212
QY 525 ILMGFSLSFGAMFSKTRVHSIFTDLKL----NKKVIKDYQLFMVVGVLAIADIIIT 580
Db 213 LTLGLVSLCYGTLAKTIRIWFIFNKPVPSTKSVIKDYALALFVSLWIDVILGI 272
QY 581 WQIADPFYRETKOLEPLHHENIDDLVIPENEY-----COSEHMTIFVSIYAKGLL 633
Db 273 FAIVEGLRGLAEVHRTSNKENIEDT-IGPTCEPHQYLYICKSGQVALTVLFYKGLL 331
QY 634 LVFGAFLAWETRHVSIPALNDSKHIGFSVNVFITCLAGAAISLVLSDRKDLVFLVLSFF 693
Db 332 QVTALIAFNTRKRVKGLDDDSKYIAAIIYTSIVLAVAAISTYTLRDYVNIYPAVVGIG 391
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QY 365 LEALRNTSEGVTPYRFFYNNEKANKLINQFOLGOMEKIGEVHSQSKHLDLSLGPKVKW 424
DQ 13 MEAIDNSSQGLGKVKFANERLGLVDIKOWSDGQVFPFAVDGADDEFKIIDSTTKGW 72
QY 425 VGTTPKDRTLIIYHSHSOVNPPTIVSASVIGVILATVFLAFNRYKQRYIKMSSPH 484
DQ 73 ---SPDLSTITERREHIS-----SILFLMSL-----FIKMSPN 106
QY 485 LNNLIIVGCMITYLSIFLGLDTLSSVAAPYICTARAWILMAGLSFGAMFSKTRWV 544
DQ 107 LNNIIAGSICTEASVIMLGRDRIIVSPDVFWLVCYKTKTLCIGFTLSFGAMFSKTRWV 166
QY 545 HSFTDLKNNKVIKDYQLEPMVGVLLAIDAIITWQIADPP-YRTEKQLEPLHNNID 603
DQ 167 HSFTIRMDRKAIDKSKLFIILGILLFIDICVLVTWAFVSPFSYTYTE---LPHIPED 222
QY 604 DVLVIPENECQSEHMTIFYSIIYAVKGLLVFGARFLAWETRHVSIPALNDSKHIGP--- 660
DQ 223 NVIIIEVEKCNHSGVFOVAVYKGVLMILGCLFANETRVHNVFALNDSKYIGTRTG 282
QY 661 --SVYNVFTCLAGAAISLVSD-----RKDLVFVLLSFF----- 693
DQ 283 QRDVQSRFVFC-----HFLDDTNVVSRCANDSKFSKTPNFTMKLFFNFKNYSGGFK 335
QY 694 -----IIFCTATLCLVFPKLVKLRNP-----QGVVDKRVKRLATLPM 733
DQ 336 NFQKLSFGGNVIFARSQV-----KKVIELARNPVGNPRAYRRGLMKSVAKTSQPM 390
QY 734 KNGR 737
DQ 391 PQPR 394

RESULT 8
Q9V309 PRELIMINARY; PRT; 1713 AA.
AC Q9V309;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE CG15274 PROTEIN.
GN GABA-B-R1 OR BG:DS00929.6 OR CG15274.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutcliffe G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Y, AND CN BW SP;
RX MEDLINE=99403001; PubMed=10471707;
RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazer R., Davis T.,
RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
RA Farfan D.E., Galle R., George R., Harris N., Hartzell G., Harvey D.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomoton M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zieran L.L., Rubin G.M.; the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003646; AAF53431.1; -
DR EMBL; AE003411; AAF44910.1; -
DR FlyBase; FBgn028924; GABA-B-R1.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000402; Na_K_beta.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 2.
KW Hypothetical protein.
SQ SEQUENCE 1713 AA; 195133 MW; 8474EBC5F9FA27AC CRC64;
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Query Match 9.5%; Score 607.5; DB 5; Length 1713;
Best Local Similarity 17.3%; Pred No. 11e-34;
Matches 269; Conservative 180; Mismatches 320; Indels 789; Gaps 40;
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QY 12 LFLLLWSTACGRATKRSY-VYAGFFPYGCVGVSNTYGRGVPYVKLALGHVNHGKIL 70
DQ 156 LLLIASPHLQGVAGVRPELHIGGIFPTA-GKGGWQGGQACMPAARLALDDVQPNLL 214
QY 71 ANYRLHMWNTQCAANAVGVKSFDDMMHSGPNKVMFLGAACTHTVDTAKAKSHWLTOL 130
DQ 215 PGFKLILNSDECEPGLGASVYNNLLYKPKQLMLL-AGCSTVCTTVAEAAKMNLI 273
QY 131 SYADTHPMFT-KDAPNFRVVPSENAFAPLALLKFNWTRVGTVTQNEPRYSPLPHNH 189
DQ 274 CYGASSPALSDRKRPFTLFRTHPSATVHNPTRIKLMKFGWSRVAILQQAEEVFI---S 329
QY 190 MYADLID--AME--VEVWETQSPVNDVAESLKKLRKDRVRIILGNFNEHFAKFACEAYKL 245
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GN Y41G9A.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Ryan E., Wohlman P., Walker C., Fielder T.;
 RT "The sequence of C. elegans cosmid Y41G9A."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006761; AAF60549.1; -
 DR InterPro; IPR001828; ANF_receptor.
 DR InterPro; IPR000337; GPCR_Mgr.
 DR Pfam; PF01094; 7tm_3; 1.
 DR Pfam; PF01094; ANF_receptor; 1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 SQ SEQUENCE 816 AA; 92251 MW; 4363D1IA46CBECA1 CRC64;

 Query Match 13.4%; Score 856.5; DB 5; Length 816;
 Best Local Similarity 28.3%; Pred. No. 3.1e-53;
 Matches 221; Conservative 164; Mismatches 327; Indels 69; Gaps 22;

 QY 49 GRGVMSVKIALGHVNEHGHKILANYRLHMMWNTDQNAAGVGVKFFDMHSGPNKVMFLG 108
 DB 11 GEACLPAVENALKDVSRLDLPGYVLNMTNHNSSOCQPLAMQQLDYLYKPKTKMLL- 69
 QY 109 AACTHTVDPAKSKWHHLTQLSVADTHP-METKDAFPNFRVVPSPNAPNAPLALLKE 167
 DB 70 TGCSPVTIVIAEAPWVKLVLTGGSPALSNRNPFTLFRTPSNANQPTRIHINEK 129
 QY 168 FNRVTGVYQNEPRYSLPHNHMVADLAMEVE---VVEQSFYNDVAESLKLREKDV 224
 DB 130 FKWKRTILMSVEEVFT---TAKDLEATARKGIRKVRQSFYGDPTDAMKTLQRQDAR 185
 QY 225 IILGNFNEHFAKAFCEAYKLDYGRAYQWLMATYSTDWNNVTQDSE---CSVEEIIATA 281
 DB 186 IIVGLFVTEARKVLCQAYHGLYGRYVFFIGWYA-DTWYIPPEHLNCTAEQWTEA 244
 QY 282 LEGAILVDLLPLSTGSDITVAGITADELYEYDRLGTEY-----SRFHGY----TYDG 331
 DB 245 AEYHFTTESVMSLRNDINPAISEMTGMQF-----QQRITQYFQKDTANVGPFPEAPLAYDA 299
 QY 332 IWAALAIQXVAEKREDLLTH-----FDYRVKDWESVLEALRNTSPGTVGPVRFYNN- 385
 DB 300 WVALALAFNCT---RNNLPISHIRENFTYDNKVYATDPLFCQVKNTSPRGVSGKVMFSDSG 356
 QY 386 ERKANILINQFQGMKEIGEYHSQSHLDLSTGKPKVWV-GKTPPKDRTLIYIEHISOVN 444
 DB 357 DRIARTQIEQMOGKGYIMGYDTTSG--DLEWYKQWQLNGKGGPPDPSTVIKKHAMTVS 414
 QY 445 PTIYIYVSASVIGVIATVFLAFNINQRYIKMSSPHNLIIYGCMTIYLSIFLG 504
 DB 415 NEFYPTILFVAGIAACVFIYLTQKHHERLIIFQSQPCNNILLIGCSLCLFSLFLG 474
 QY 505 L--DTTLSSVAAPPYICTARAILMAGFSLSGFAMFSKTRVHSHFTD-----LKLKKK 556
 DB 475 LPSDDISISESLFPLLCARVITLLFGFTFAYGSMFAKVIWVHRMGATENOQLASRKDE 534

 QY 557 VIKDYQLFMVGVGLLAIDIAIITWQIADPFYRETKQLEPLH--HENIDDLVLPENEYC 614
 DB 535 PISSKFFYVIAALFAVDVFCVFWVLIDPLHL-TEQKPLPTPADSEDEIMPVLQOC 593
 QY 615 QSEHTMTFVSIYAYKGLLVFGAFLAWETRVHSVPALNDSKHIGFSVYNVFI-TCLAGA 673
 DB 594 OSNQOEVMGIIIMGFKCLLVFGTFLSYETRNKLRFINDSRFVGLAIYNVAVMTLVTAP 653
 QY 674 AISLVLSORKDLVFLVLLSFFIIFCTATLCLVFVKLVKRNQGVVDKRVATLRP-- 731
 DB 654 VVTLLIHGKVDANFAFISL-----TVGLIYGPKIRHIIKVPVSADEIQLNGNVGPGV 705
 QY 732 MSKNG-----RRDSSVCEQLRLDYKNTNCRPKALMEKENELQALIRKLGPEARKW 784
 DB 706 MSKVDKRYDMLKKNETLQIQIEEKKERLHECKERLEELTKNSETEDMNAQLLCENDKQ 765
 QY 785 I 785
 DB 766 I 766

 RESULT 7
 Q23442 PRELIMINARY; PRT; 402 AA.
 AC Q23442:
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE COSMID ZK180.
 GN ZK180.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Coulson A.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Pauley A., Le T.T.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U58748; AAB52965.1; -
 DR InterPro; IPR000337; GPCR_Mgr.
 DR InterPro; IPR001064; Crystallin.
 DR Pfam; PF00003; 7tm_3; 1.
 DR PROSITE; PS0225; CRYSTALLIN_BETACAMMA; UNKNOWN_1.
 DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
 SQ SEQUENCE 402 AA; 45577 MW; D48DF0916CB4EFEE CRC64;

 Query Match 10.1%; Score 646.5; DB 5; Length 402;
 Best Local Similarity 35.1%; Pred. No. 1.6e-38;
 Matches 149; Conservative 68; Mismatches 114; Indels 93; Gaps 11;

RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
DR EMBL; AE003588; AAF51465.2;
DR FlyBase; FBgn0031275; GABA-B-R3.
DR InterPro; IPR001828; ANF_Receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR000005; HTHArac.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR PRINTS; GPCR0248; GPCRMR.
DR PROSITE; PS00259; G_PROTEIN_RECEPTOR_F3_4; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
SQ SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;

Query Match 19.2%; Score 1229; DB 5; Length 1305;
Best Local Similarity 30.5%; Pred. No. 7.1e-80;
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps 34;

QY 48 TGRGVP-----SVKALGHNVEHGKILANYRLHMMWNTQCNAAYGVKSFDDMMHSG 100
DB 163 TSGRPDPGLSELGAATMAVEHINRK-RLLPGYTLVNTDQCDDPGVGVDREFFHAIYQ 221
QY 101 PN--KVMFLFGAACHVTDPIAKSKHHWLTQLSYADTHPMFT-KDAFPNFRVVPSENAF 157
DB 222 PSTRMVMLLGSACSEVTESLAKVVPYWNIVQSFSTSPALSDDREFFPYFYRTVAPDSSH 281
QY 158 NAPRLALLKEFNWRTGVYQNEPRYSLPHNHMVDLDAVEVEVETQSF-VNDVAESLK 216
DB 282 NPATIAFIRKFGMGVTTFTSQNEVHSLAVNNLVTELEAANISCAATITFAATDFKEQLL 341
QY 217 KLRKEDVRIILGNFNEHFAKFAECAYKLDYGRAYQWLIMATYTDWNNVTQDSECVSE 276
DB 342 LLRETDRILIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWM-PDORTACSNH 400
QY 277 EIATALEGAILVDLLPLSTSGDITVAGITADEYLVEYDRLGRTEYGRFHG----- 326
DB 401 ELQLAIVENLIVVSTHNSIVGNVSYGLNNHMF---NSQLR-KQSAQFHGDDGFGSGYGS 456
QY 327 -----TYDGIWAAALAIQVVAE----- 344
DB 457 RISTAAQTSDRRRRRGVGTSGHLPPEAISQVAPQYDAVMAIALALRAAEHWRN 516
QY 345 KREDLLTHFDYRVKD--WESVLEALRNTSEFVTPGVRFYNNERNKANILINQFOLGOME 402
DB 517 EEQSKLDGDFYTRSDMAWE--FLQMGKHLFLGVSGPVSFSCPDRVGTAFYQIQIGLLE 574
QY 403 KIGBYHSQKSHLDLSLG--KPVKWGKTPPKDRTLIYIEHSQVNPPTIIVSASVIGVI 460
DB 575 PVALYYPATDALDFRCPRCPRVKHSQVPIAKRVFKLRVATIAPLAFYTIATLTSVGIA 634
QY 461 IATVFLAFNIQRQYIKMSSPHLNNLIIVGCMITYLSIFLGLD--TTLSSVAAPFYI 518
DB 635 LAIAFLAFNHFRLKAIKALSPKLSNTAVGCFIVYATVILLLGDHDLTLPDAEDSFATV 694
QY 519 CTARAWILMAQFSLSFGAMFSTKVRVSHIF--TDLKLNKKVIKDYQLFMWGVGLLAIDIA 576
DB 695 CTARVYLLSAGFSLAFSGMFAKTRVHRIFRTGVSFVKDMQLQDLILLVGLLIVDAL 754
QY 577 IITWQIADPYRETQKLEPLHENID-----DVLVIPENEYCOSEHMTIFVSIYYAYK 630
DB 755 LVTLWVTDPMERH-----LHNLTEISATDRSVYQPVQVEVCRSQHTQTWLSVLYAYK 808
QY 631 GLLLVGFAFLAWETRHSIPALNDSKHGFSVYVNTFCLAGAAISLVLSDRKDLVFLVLL 690
DB 809 GLLLVGVYMAWETRHKVIPALNDSQYIGSVSYVITSAIVVVLANLISERVTLAFITTI 868
QY 691 SFFLIETCTATCLVFPVKLVEL-KRNPQGVVDKVRVATLRPMKNGRR---DSSVCEL 745
DB 869 TALILTSTATCLLFIPLKLDHIAWN--DIIDPVIHSMGLKMECNTRFRVVDRR--EL 924

QY 746 EORLDRVKNTRCRRKALMEKENELQAL---IRKLGPEARKWIDGVTCGGSNW-----G 797
DB 925 QTRV-EVQN---RVYK-----KEIQALDAEIRKRLLESGLTSTTSTSSSTSLTGG 974
QY 798 SELEPILNDIVRLSAPPVRRREMPSTVTMTSVDSTVTHVEMDN---SFSVSVQSTVMA 854
DB 975 GHLKP-----ELVTVSGISQTPAASKNRTSPISGILPNLL 1010
QY 855 PSLPPKKKQKOSIVEHHSHAPAPTMQPIQOOLOOHQHOQOQOHLQOQOHOQOQOQOQ 914
DB 1011 SVLPP-----VIPRASWPSAEYMQIPMRRSVT--FASQPLEEACLPADDLINLRLAHQ 1062
QY 915 QOOHHHRL--EKRNSVSAQTDDNIGSIYSTACKRSGDCSSMRERRQSTASRHYDGSQ 972
DB 1063 QATEAKTGLINLRGIFSTSSNKGSTASLADQK---LKAAPKSHMGLFTLRIPS-SQ 1118
QY 973 TPTARPKYSSSHRNSTNISTQSELSNMCPSKSPSTPAVIKTPTASDH 1021
DB 1119 TASCNAIYNNPQDSIPSEASSHPNGNHLKPIHRGS---LTKSGTHLDH 1164

RESULT 4
Q9BML5 PRELIMINARY; PRT; 1305 AA.
AC Q9BML5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE METABOTROPIC GABA-B RECEPTOR SUBTYPE 3.
GN GABA-B-R3.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11168554;
RA Mezler M., Muller T., Raming K.;
RT "Cloning and functional expression of GABA-B receptors from
RT *Drosophila*."
RL Eur. J. Neurosci. 13:477-486(2001).
DR EMBL; AF318274; AAK13422.1; -.
KW Receptor.
SQ SEQUENCE 1305 AA; 143701 MW; 8BBFA80F0E9BEADD CRC64;

Query Match 19.2%; Score 1229; DB 5; Length 1305;
Best Local Similarity 30.5%; Pred. No. 7.1e-80;
Matches 326; Conservative 191; Mismatches 390; Indels 162; Gaps 34;

QY 48 TGRGVP-----SVKALGHNVEHGKILANYRLHMMWNTQCNAAYGVKSFDDMMHSG 100
DB 163 TSGRPDPGLSELGAATMAVEHINRK-RLLPGYTLVNTDQCDDPGVGVDREFFHAIYQ 221
QY 101 PN--KVMFLFGAACHVTDPIAKSKHHWLTQLSYADTHPMFT-KDAFPNFRVVPSENAF 157
DB 222 PSTRMVMLLGSACSEVTESLAKVVPYWNIVQSFSTSPALSDDREFFPYFYRTVAPDSSH 281
QY 158 NAPRLALLKEFNWRTGVYQNEPRYSLPHNHMVDLDAVEVEVETQSF-VNDVAESLK 216
DB 282 NPATIAFIRKFGMGVTTFTSQNEVHSLAVNNLVTELEAANISCAATITFAATDFKEQLL 341
QY 217 KLRKEDVRIILGNFNEHFAKFAECAYKLDYGRAYQWLIMATYTDWNNVTQDSECVSE 276
DB 342 LLRETDRILIGSFQELAPQILCEAYRLRMFGADYAWILHESMGAPWM-PDORTACSNH 400
QY 277 EIATALEGAILVDLLPLSTSGDITVAGITADEYLVEYDRLGRTEYGRFHG----- 326
DB 401 ELQLAIVENLIVVSTHNSIVGNVSYGLNNHMF---NSQLR-KQSAQFHGDDGFGSGYGP 456
QY 327 -----TYDGIWAAALAIQVVAE----- 344

DR Pfam: PF01094; ANF_receptor; 2.
DR PROSITE: PS0259; G_PROTEIN_RECPT_F3_4; 1.
SQ SEQUENCE 1221 AA; 138123 MW; A57A9954F31FOA05 CRC64;

Query Match 99.8%; Score 6395.5; DB 5; Length 1221;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1219; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MFRPSFPFASLLFLLWSTACGRTAKRSVDYIAGFFPYGDSVNSYTGRCVMPKVLAL 60
DB 1 MFRPSFPFASLLFLLWSTACGRTAKRSVDYIAGFFPYGDSVNSYTGRCVMPKVLAL 60

QY 61 GHVNEHGKILANTRLHWNNDTCNAAGVGVKSPFDMHSGPNKVMYLGAACTHTVTDPIAK 120
DB 61 GHVNEHGKILANTRLHWNNDTCNAAGVGVKSPFDMHSGPNKVMYLGAACTHTVTDPIAK 120

QY 121 ASKHWHLTQLSYADTHPMFTKDAFPNFRVVPVSENAFNAPLALLKEFNWTRVGTVYQNE 180
DB 121 ASKHWHLTQLSYADTHPMFTKDAFPNFRVVPVSENAFNAPLALLKEFNWTRVGTVYQNE 180

QY 181 PRYSLPHNHMVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFC 240
DB 181 PRYSLPHNHMVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHFARKAFC 240

QY 241 EAYKLDYGRAYOWLIMATYSTDMWNTQDSECSVEEIAALEGAILVDLLPLSTSGDIT 300
DB 241 EAYKLDYGRAYOWLIMATYSTDMWNTQDSECSVEEIAALEGAILVDLLPLSTSGDIT 300

QY 301 VAGITADEYLVEYDLRGTEYSRFGHYTDGIIWAALAIQYVAEKREDLLTHFYRYKDW 360
DB 301 VAGITADEYLVEYDLRGTEYSRFGHYTDGIIWAALAIQYVAEKREDLLTHFYRYKDW 360

QY 361 ESFLEALRNTSEGVTPGVRFYNNERKANILINQFOLGOMEKIGEYHSQKSHLDLSGK 420
DB 361 ESFLEALRNTSEGVTPGVRFYNNERKANILINQFOLGOMEKIGEYHSQKSHLDLSGK 420

QY 421 PVKWGKTPPKDRTLIYIEHSQVNPTIYIVSASVIGVIAATVFLAFNIKRYNORYIKM 480
DB 421 PVKWGKTPPKDRTLIYIEHSQVNPTIYIVSASVIGVIAATVFLAFNIKRYNORYIKM 480

QY 481 SSPHLNLIIVGCMITVLSIFIGLDITLSSVAAPFICTARAWILMAGFSLSGAMFSK 540
DB 481 SSPHLNLIIVGCMITVLSIFIGLDITLSSVAAPFICTARAWILMAGFSLSGAMFSK 540

QY 541 TWRVHSIFTDLKLNKKVYKQYQFMVGVLLAIDIAITWQIADPPFYRETKQLEPLHHE 600
DB 541 TWRVHSIFTDLKLNKKVYKQYQFMVGVLLAIDIAITWQIADPPFYRETKQLEPLHHE 600

QY 601 NIDDLVLPENEXCQSEHMTIFVSIYAYKGLLVFGAFLAWETRHYSPALNDSKHIGF 660
DB 601 NIDDLVLPENEXCQSEHMTIFVSIYAYKGLLVFGAFLAWETRHYSPALNDSKHIGF 660

QY 661 SVYNVFTCLAGAAISLVSDRDLVFLVLSFFIIFCTTATCLVLFPVKLVYELKRNQGV 720
DB 661 SVYNVFTCLAGAAISLVSDRDLVFLVLSFFIIFCTTATCLVLFPVKLVYELKRNQGV 720

QY 721 VDKRRVATLPMKNGRDSVCELEORLDVKNTRFRKALMEKENELQALIRKLGE 780
DB 721 VDKRRVATLPMKNGRDSVCELEORLDVKNTRFRKALMEKENELQALIRKLGE 780

QY 781 ARKWIDGVCTGSGVSELEPILNDDIVLSAPPVVRREMPSTT-VTEMTSDVSTSHV 839
DB 781 ARKWIDGVCTGSGVSELEPILNDDIVLSAPPVVRREMPSTT-VTEMTSDVSTSHV 840

QY 840 EMDNSFVSVQSTVMAPSLPKKKQKQSVHEHSHAPATMMQPTIOQQLQHQHQMOQ 899
DB 841 EMDNSFVSVQSTVMAPSLPKKKQKQSVHEHSHAPATMMQPTIOQQLQHQHQMOQ 900

QY 900 HLOQOQHQMOQOQOQOQOQHHRHLEKNSVSAQTDNIGSTITAGKRSKSGDCSMRER 959
DB 901 HLOQOQHQMOQOQOQOQOQHHRHLEKNSVSAQTDNIGSTITAGKRSKSGDCSMRER 960

QY 960 QSTASRHRDYSQSQTPTARPKYSSSHRNSTNTSTQSELSNMCPSKSPSTPAVKTPTAS 1019
DB 961 QSTASRHRDYSQSQTPTARPKYSSSHRNSTNTSTQSELSNMCPSKSPSTPAVKTPTAS 1020

QY 1020 DHRRTSMGSALKSNFVVSQSLDWDHTTLSHAKQSPRNYASPORCAEHGGHGTDPN 1079
DB 1021 DHRRTSMGSALKSNFVVSQSLDWDHTTLSHAKQSPRNYASPORCAEHGGHGTDPN 1080

QY 1080 TTSPTQSRVSEKNRNKRPKPKGTVCQSETDSEERDPPNPSQPCVOPRKVRSRNTQH 1139
DB 1081 TTSPTQSRVSEKNRNKRPKPKGTVCQSETDSEERDPPNPSQPCVOPRKVRSRNTQH 1140

QY 1140 AAHHSSNPVADPKORSRQKQDSIYGASSETELLEGETAILPIFRKLLTEKSPNYRG 1199
DB 1141 AAHHSSNPVADPKORSRQKQDSIYGASSETELLEGETAILPIFRKLLTEKSPNYRG 1200

QY 1200 RSAGVQSCPNISIKCDIVEYL 1220
DB 1201 RSAGVQSCPNISIKCDIVEYL 1221

RESULT 3
Q9VPS7 PRELIMINARY; PRT; 1305 AA.

ID Q9VPS7
AC Q9VPS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG3022 PROTEIN.
GN GABA-B-R3 OR CG3022.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20195006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balwle R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Besson D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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QY 181 PRYSLPHNHVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHPARKAFC 240
Db 181 PRYSLPHNHVADLDAMEVEVETQSFVNDVAESLKKLREKDVRIILGNFNEHPARKAFC 240
QY 241 EAYKLDYGRAYOWLIIMATYSTDMWNVTQDSECSVEEETATALEGAILVDLLPLSTSGDIT 300
Db 241 EAYKLDYGRAYOWLIIMATYSTDMWNVTQDSECSVEEETATALEGAILVDLLPLSTSGDIT 300
QY 301 VAGITADEYLVEYDRLRGTEYSRPHGTYDGIWAAALAIQVVAEKREDLLTHFDYRVKDW 360
Db 301 VAGITADEYLVEYDRLRGTEYSRPHGTYDGIWAAALAIQVVAEKREDLLTHFDYRVKDW 360
QY 361 ESYFLEALRNTSEGVTPVRFYNNERKANLIIQFOLGOMEKICEYHSQKSHDLDSLKG 420
Db 361 ESYFLEALRNTSEGVTPVRFYNNERKANLIIQFOLGOMEKICEYHSQKSHDLDSLKG 420
QY 421 PVKVGKTPPKDRTLIIIEHSQVNPITYIVSASASVIGVIIATVFLAFNIYRNQRYIKM 480
Db 421 PVKVGKTPPKDRTLIIIEHSQVNPITYIVSASASVIGVIIATVFLAFNIYRNQRYIKM 480
QY 481 SSPHLNLIIVGCMITVLSIIFLGLDITLSSVAAPFYICTARAWILMAGFSLSGAMEFSK 540
Db 481 SSPHLNLIIVGCMITVLSIIFLGLDITLSSVAAPFYICTARAWILMAGFSLSGAMEFSK 540
QY 541 TWRVHSITFDLKNKKVICYOLFPMVGVLLAIDIAITTTQIADPPFYRETKOLEPLHHE 600
Db 541 TWRVHSITFDLKNKKVICYOLFPMVGVLLAIDIAITTTQIADPPFYRETKOLEPLHHE 600
QY 601 NIDDLVLPENECQSHMTIFVSIYAYKGLLVGFAGFLAWETHVSIIPALNDSKHITGF 660
Db 601 NIDDLVLPENECQSHMTIFVSIYAYKGLLVGFAGFLAWETHVSIIPALNDSKHITGF 660
QY 661 SVYNVFTITLAGAASLVLSDRKDLVFLVLSFFIIFCTTATLCLVFPKLVKLKRNPOGV 720
Db 661 SVYNVFTITLAGAASLVLSDRKDLVFLVLSFFIIFCTTATLCLVFPKLVKLKRNPOGV 720
QY 721 VDKRVATLRPMKNGRRDSSVCELEORLDRVKNTRCFRKALMEKENELQALIRKLGP 780
Db 721 VDKRVATLRPMKNGRRDSSVCELEORLDRVKNTRCFRKALMEKENELQALIRKLGP 780
QY 781 ARKWIDGVTCTGSGNVGSELEPILNDDIVLSAPPVREMPSTVTMTSVDSTSTHVE 840
Db 781 ARKWIDGVTCTGSGNVGSELEPILNDDIVLSAPPVREMPSTVTMTSVDSTSTHVE 840
QY 841 MDNSFVSQSVTMAPSLPPKKKQSIIVEHHSHAPAPTMMPQIQOOLQOHLQOHOQOQO 900
Db 841 MDNSFVSQSVTMAPSLPPKKKQSIIVEHHSHAPAPTMMPQIQOOLQOHLQOHOQOQO 900
QY 901 LQOQOHOQOQOQOQOQOHHHLEKRNVSQAOTDDNIGSTITAGKRSGGDCSSMRERQ 960
Db 901 LQOQOHOQOQOQOQOQOHHHLEKRNVSQAOTDDNIGSTITAGKRSGGDCSSMRERQ 960
QY 961 STASRHYDGSQPTAPRKYSSSHRSNSTNISTSQSELSNMCPSKSPPAVTKPTASD 1020
Db 961 STASRHYDGSQPTAPRKYSSSHRSNSTNISTSQSELSNMCPSKSPPAVTKPTASD 1020
QY 1021 HRTSMGSAKSNFVVSQSLMDWTHLTSKAKQOSPRNYASQPCAEHHGGHGMITYDPT 1080
Db 1021 HRTSMGSAKSNFVVSQSLMDWTHLTSKAKQOSPRNYASQPCAEHHGGHGMITYDPT 1080
QY 1081 TSPIQRSVSEKNNKRPKQKGTVCQSETDSERDPPPNQPCVQPRKVSRSNTQHA 1140
Db 1081 TSPIQRSVSEKNNKRPKQKGTVCQSETDSERDPPPNQPCVQPRKVSRSNTQHA 1140
QY 1141 AHHSSPNVAPDKQSRQKQDSIIYGASSETELLEGETAILPIFRKLLTEKSPNYRGR 1200
Db 1141 AHHSSPNVAPDKQSRQKQDSIIYGASSETELLEGETAILPIFRKLLTEKSPNYRGR 1200
QY 1201 SAVGQSCPNIISIKDIVEYL 1220
Db 1201 SAVGQSCPNIISIKDIVEYL 1220
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RESULT 2
QY133
ID QY133 PRELIMINARY; PRT: 1221 AA.
AC QY133;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BCDNA:GH07312 PROTEIN.
GN GABA-B-R2 OR BCDNA:GH07312 OR CG6706.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brotter P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Feiraz C., Ferreira S., Fleischmann W.,
RA Fouts R.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
RN [2]
RP Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agayani A., Arcina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA Celniker S.E.;
RT "Full length Drosophila melanogaster cDNA sequence.";
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE003736; AAF55916.1; -.
DR EMBL; AF145639; AAD38614.1; -.
DR FlyBase; FBgn0027575; GABA-B-R2.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR Pfam; PF00003; 7tm_3; 1.
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 30, 2002, 10:00:48 ; Search time 74.36 Seconds
(without alignments)
2399.842 Million cell updates/sec

Title: US-09-715-962-4
Perfect score: 6409
Sequence: 1 MFRPSWPFASLLFLLLWST.....SANGQSCPNIKIDIVEYL 1220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6409	100.0	1220	5 Q9BML6	Q9bml6 drosophila
2	6395.5	99.8	1221	5 Q9Y133	Q9y133 drosophila
3	1229	19.2	1305	5 Q9VPS7	Q9vps7 drosophila
4	1229	19.2	1305	5 Q9BML5	Q9bml5 drosophila
5	1186.5	18.5	840	5 Q9BML7	Q9bml7 drosophila
6	856.5	13.4	816	5 Q9N502	Q9n502 caenorhabdi
7	646.5	10.1	402	5 Q23442	Q23442 caenorhabdi
8	607.5	9.5	1713	5 Q9V309	Q9v3q9 drosophila
9	418	6.5	528	5 Q96954	Q96954 geodia cydo
10	329.5	5.1	153	11 Q9QV85	Q9qy85 rattus norv
11	304	4.7	1188	13 Q98UC5	Q98uc5 gallus gall
12	303	4.7	1242	13 Q98UC4	Q98uc4 gallus gall
13	296	4.6	1156	13 Q98UC6	Q98uc6 gallus gall
14	285.5	4.5	976	5 Q9V485	Q9v485 drosophila
15	281	4.4	983	11 Q62916	Q62916 rattus norv
16	266.5	4.2	738	5 Q9V403	Q9v4u3 drosophila
17	265	4.1	1199	11 Q9EVP6	Q9epv6 mus musculu
18	246.5	3.8	941	10 Q9SMD9	Q9swd9 arabidopsis
19	244	3.8	872	4 Q9H3N6	Q9h3n6 homo sapien

20	241	3.8	962	10	O23048	O23048 arabidopsis
21	240	3.7	879	11	Q9QYS2	Q9qys2 mus musculu
22	238	3.7	838	5	Q9YOC9	Q9yoc9 dictyosteli
23	237	3.7	921	10	Q9SDQ4	Q9sdq4 arabidopsis
24	237	3.7	923	10	Q9ZV68	Q9zv68 arabidopsis
25	235	3.7	253	5	Q23443	Q23443 caenorhabdi
26	230	3.6	877	13	Q9PW88	Q9pw88 carassius a
27	229.5	3.6	848	13	Q9S553	Q9s553 carassius a
28	228	3.6	1104	13	Q9W6R6	Q9w6r6 fugu rubrip
29	224	3.5	1480	5	Q9V583	Q9v583 drosophila
30	223	3.5	877	4	Q9UGT0	Q9ugt0 homo sapien
31	222	3.5	507	13	Q9DG04	Q9dg04 xenopus lae
32	222	3.5	1267	5	Q93564	Q93564 caenorhabdi
33	221	3.4	1529	5	Q9GQC2	Q9gc2 dictyosteli
34	219.5	3.4	912	10	Q9C561	Q9c561 arabidopsis
35	218.5	3.4	925	10	O65498	O65498 arabidopsis
36	218.5	3.4	2067	11	Q9JL19	Q9jl19 mus musculu
37	218	3.4	1920	5	Q9V982	Q9v982 drosophila
38	213.5	3.3	953	10	Q9ZV67	Q9zv67 arabidopsis
39	212	3.3	870	5	Q9N4T8	Q9n4t8 caenorhabdi
40	211	3.3	550	5	Q9VN76	Q9vn76 drosophila
41	210.5	3.3	1010	5	O18346	O18346 drosophila
42	209	3.3	912	10	Q9SES5	Q9ses5 brassica na
43	207	3.2	589	4	Q9UGS9	Q9ugs9 homo sapien
44	207	3.2	853	4	Q9NTG8	Q9ntg8 homo sapien
45	207	3.2	1186	5	Q21227	Q21227 caenorhabdi

ALIGNMENTS

RESULT 1

ID Q9BML6 PRELIMINARY; PRT; 1220 AA.
AC Q9BML6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE METABOTROPIC GABA-B RECEPTOR SUBTYPE 2.
GN GABA-B-R2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11168554;
RA Mezler M., Muller T., Ramling K.;
RT "Cloning and functional expression of GABA-B receptors from Drosophila";
RL Eur. J. Neurosci. 13:477-486(2001).
DR EMBL; AF318273; AAK13421.1; -;
KW Receptor.
SQ SEQUENCE 1220 AA; 137976 MW; 2B33DA2C1A1BDA8B CRC64;

Query Match 100.0%; Score 6409; DB 5; Length 1220;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFRPSWPFASLLFLLLWSTACGRTAKRSVDYIAGFFPYGDGVNSYTGRCVMPKSLAL 60
Db 1 MFRPSWPFASLLFLLLWSTACGRTAKRSVDYIAGFFPYGDGVNSYTGRCVMPKSLAL 60

QY 61 GHVNEHGKILANRLHWNNDTCNAAVGVKSFDDMHSGPNKVMFGAACTHTVDTPIAK 120
Db 61 GHVNEHGKILANRLHWNNDTCNAAVGVKSFDDMHSGPNKVMFGAACTHTVDTPIAK 120

QY 121 ASKHWHULTQISYADTHPMFTKDAFFNFRVVPSENAFNAPRLALLKEFNWTRVGTVTYQNE 180
Db 121 ASKHWHULTQISYADTHPMFTKDAFFNFRVVPSENAFNAPRLALLKEFNWTRVGTVTYQNE 180